

NS.txt SEQUENCE LISTING

```
<110> BETTER, Marc D.
      HORWITZ, Arnold H.
<120> HUMAN ENGINEERED TO ANTIBODIES TO EP-CAM
<130> 117791-072
<140> US 10/816,276
<141> 2004-03-31
<150> US 60/459,334
<151> 2003-03-31
<160> 61
<170> PatentIn version 3.2
<210> 1
<211> 720
<212> DNA
<213> Homo sapiens
<220>
<221> misc_feature
<223> Mouse Human Chimeric Light Chain DNA and Protein
<220>
<221> CDS
<222> (1)..(717)
<220>
<221> mat_peptide
<222> (61)..()
<400> 1
                                                                                        48
      atg agg ttc tct gct cag ctt ctg ggg ctg ctt gtg ctc tgg atc cct
      Met Arg Phe Ser Ala Glm Leu Leu Gly Leu Leu Val Leu Trp Ile Pro
                              -15
                                                     -10
      -20
      gga tcc act gca gat att gtg atg acg cag gct gca ttc tcc aat cca
Gly Ser Thr Ala Asp Ile Val Met Thr Gln Ala Ala Phe Ser Asn Pro
                                                                                        96
      gtc act ctt gga aca tca ggt tcc atc tcc tgc agg tct agt aag agt
                                                                                       144
      Val Thr Leu Gly Thr Ser Gly Ser Ile Ser Cys Arg Ser Ser Lys Ser
15 20 25
      ctc cta cat agt aat ggc atc act tat ttg tat tgg tat ctg cag aag
                                                                                       192
      Leu Leu His Ser Asn Gly Ile Thr Tyr Leu Tyr Trp Tyr Leu Gln Lys
                                                          40
                                   35
      cca ggc cag tct cct cag ctc ctg att tat cag atg tcc aac ctt gcc
Pro Gly Gln Ser Pro Gln Leu Leu Ile Tyr Gln Met Ser Asn Leu Ala
                                                                                       240
      45
                                                     55
                              50
      tca gga gtc cca gac agg ttc agt agc agt ggg tca gga act gat ttc
                                                                                       288
      Ser Gly Val Pro Asp Arg Phe Ser Ser Ser Gly Ser Gly Thr Asp Phe
                         65
                                                70
                                                                                       336
      aca ctg aga atc agc aga gtg gag gct gag gat gtg ggt gtt tat tac
      Thr Leu Arg Ile Ser Arg Val Glu Ala Glu Asp Val Gly Val Tyr Tyr
      tgt gct caa aat cta gaa ctt cct cgg acg ttc ggt gga ggc acc aag
Cys Ala Gln Asn Leu Glu Leu Pro Arg Thr Phe Gly Gly Gly Thr Lys
                                                                                       384
                                                              105
                                       100
                95
                                                                                       432
      ctt gag atg aaa cga act gtg gct gca cca tct gtc ttc atc ttc ccg
      Leu Glu Met Lys Arg Thr Val Ala Ala Pro Ser Val Phe Ile Phe Pro
                                             Page 1
```

```
NS.txt
            110
                                     115
                                                              120
       cca tct gat gag cag ttg aaa tct gga act gcc tct gtt gtg tgc ctg
Pro Ser Asp Glu Gln Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu
                                                                                             480
       125
                                                        135
                                130
       ctg aat aac ttc tat ccc aga gag gcc aaa gta cag tgg aag gtg gat
                                                                                             528
       Leu Asn Asn Phe Tyr Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp
       aac gcc ctc caa tcg ggt aac tcc cag gag agt gtc aca gag cag gac
Asn Ala Leu Gln Ser Gly Asn Ser Gln Glu Ser Val Thr Glu Gln Asp
                                                                                             576
                                               165
                                                                       170
       agc aag gac agc acc tac agc ctc agc agc acc ctg acg ctg agc aaa
Ser Lys Asp Ser Thr Tyr Ser Leu Ser Ser Thr Leu Thr Leu Ser Lys
                                                                                             624
                 175
                                          180
                                                                  185
       gca gac tac gag aaa cac aaa gtc tac gcc tgc gaa gtc acc cat cag
Ala Asp Tyr Glu Lys His Lys Val Tyr Ala Cys Glu Val Thr His Gln
                                                                                             672
                                     195
                                                              200
       ggc ctg agc tcg ccc gtc aca aag agc ttc aac agg gga gag tgt tag
Gly Leu Ser Ser Pro Val Thr Lys Ser Phe Asn Arg Gly Glu Cys
                                                                                            720
                                210
                                                        215
<210> 2
<211> 239
<212> PRT
<213> Homo sapiens
<400> 2
       Met Arg Phe Ser Ala Gln Leu Leu Gly Leu Leu Val Leu Trp Ile Pro
                               -15
                                                        -10
       Gly Ser Thr Ala Asp Ile Val Met Thr Gln Ala Ala Phe Ser Asn Pro
                     -1 1
                                                                       10
       Val Thr Leu Gly Thr Ser Gly Ser Ile Ser Cys Arg Ser Ser Lys Ser 15 20 25 ___
       Leu Leu His Ser Asn Gly Ile Thr Tyr Leu Tyr Trp Tyr Leu Gln Lys
30 40
                                     35
       Pro Gly Gln Ser Pro Gln Leu Leu Ile Tyr Gln Met Ser Asn Leu Ala
                                50
                                                        55
       Ser Gly Val Pro Asp Arg Phe Ser Ser Ser Gly Ser Gly Thr Asp Phe
                           65
                                                   70
       Thr Leu Arg Ile Ser Arg Val Glu Ala Glu Asp Val Gly Val Tyr Tyr
                                              85
       Cys Ala Gln Asn Leu Glu Leu Pro Arg Thr Phe Gly Gly Thr Lys
95 100 105
                 95
                                          100
       Leu Glu Met Lys Arg Thr Val Ala Ala Pro Ser Val Phe Ile Phe Pro
                                     115
                                                             120
       Pro Ser Asp Glu Gln Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu
                                                        135
                                130
       Leu Asn Asn Phe Tyr Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp
145 150 155
       Asn Ala Leu Gln Ser Gly Asn Ser Gln Glu Ser Val Thr Glu Gln Asp
                                                                       170
                      160
                                              165
       Ser Lys Asp Ser Thr Tyr Ser Leu Ser Ser Thr Leu Thr Leu Ser Lys
                 175
                                         180
                                                                  185
       Ala Asp Tyr Glu Lys His Lys Val Tyr Ala Cys Glu Val Thr His Gln
                                    195
           190
                                                            200
       Gly Leu Ser Ser Pro Val Thr Lys Ser Phe Asn Arg Gly Glu Cys
                                210
                                                        215
<210> 3
<211> 1398
<212> DNA
<213> Homo sapiens
<220>
```

```
<221> misc_feature
<223> Mouse-Human chimeric Heavy Chain DNA and Protein Sequence
<220>
<221> CDS
<222> (1)..(1395)
<220>
<221> mat_peptide
<222> (58) ..()
<400> 3
       atg gct tgg gtg tcc acc ttg cta ttc ctg atg gca gct gcc caa agt
                                                                                                    48
       Met Ăla Trp Val Ser Thr Leu Leu Phe Leu Met Ala Ala Ala Gln Ser
                            -15
                                                       -10
       gcc caa gca cag atc cag ttg gtg cag tct gga cct gag ctg aag aag
Ala Gln Ala Gln Ile Gln Leu Val Gln Ser Gly Pro Glu Leu Lys Lys
                                                                                                    96
       cct gga gag aca gtc aag atc tcc tgc aag gct tct gga tat acc ttc
                                                                                                   144
        Pro Gly Glu Thr Val Lys Ile Ser Cys Lys Ala Ser Gly Tyr Thr Phe
                                       20
                                                                                                   192
        aca aaa tat gga atg aac tgg gtg aag cag gct cca gga aag ggt tta
        Thr Lys Tyr Gly Met Asn Trp Val Lys Gln Ala Pro Gly Lys Gly Leu
       aag tgg atg ggc tgg ata aac acc tac act gaa gag cca aca tat ggt
Lys Trp Met Gly Trp Ile Asn Thr Tyr Thr Glu Glu Pro Thr Tyr Gly
                                                                                                   240
                             50
       gat gac ttc aag gga cgg ttt gcc ttc tct ttg gaa acc tct gcc agc
                                                                                                   288
       Āsp Āsp Phe Lyš Ğly Arg Phe Āla Phe Ser Leu Ğlu Thr Ser Āla Ser
                                                                            75
                       65
                                                  70
                                                                                                   336
       act gcc aat ttg cag atc aac aac ctc aaa agt gag gac acg gct aca
       Thr Ala Asn Leu Gln Ile Asn Asn Leu Lys Ser Glu Asp Thr Ala Thr
                                            85
       tat ttc tgt gca aga ttt ggc tct gct gtg gac tac tgg ggt caa gga
Tyr Phe Cys Ala Arg Phe Gly Ser Ala Val Asp Tyr Trp Gly Gln Gly
                                                                                                   384
                                       100
                                                                  105
       acc tcg gtc acc gtc tcc tca gcc agc aca aag ggc cca tcg gtc ttc
Thr Ser Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val Phe
                                                                                                   432
        110
                                  115
                                                            120
       ccc ctg gca ccc tcc tcc aag agc acc tct ggg ggc aca gcg gcc ctg
Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala Leu
                                                                                                   480
                             130
                                                       135
       ggc tgc ctg gtc aag gac tac ttc ccc gaa ccg gtg acg gtg tcg tgg
                                                                                                   528
       ĞÎY CŸS LEŨ VAÎ LYS ÂSP TYr Phe Pro ĞÎU Pro VAÎ Thr VAÎ Ser Trp
                                                  150
                                                                                                   576
       aac tca ggc gcc ctg acc agc ggc gtg cac acc ttc ccg gct gtc cta
Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val Leu
                  160
                                            165
                                                                       170
       cag tcc tca gga ctc tac tcc ctc agc agc gtg gtg acc gtg ccc tcc Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro Ser
                                                                                                   624
                                       180
                                                                  185
            175
       agc agc ttg ggc acc cag acc tac atc tgc aac gtg aat cac aag ccc
                                                                                                   672
       Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His Lys Pro
                                  195
                                                            200
       agc aac acc aag gtg gac aag aga gtt gag ccc aaa tct tgt gac aaa
Ser Asn Thr Lys Val Asp Lys Arg Val Glu Pro Lys Ser Cys Asp Lys
                                                                                                   720
                             210
                                                       215
       act cac aca tgc cca ccg tgc cca gca cct gaa ctc ctg ggg gga ccg
Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly Pro
                                                                                                   768
                                                                            235
                                                  230
                                                                                                   816
       tca gtc ttc ctc ttc ccc cca aaa ccc aag gac acc ctc atg atc tcc
       Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser
                                            245
                                                                       250
```

Page 3

									NS	.txt							
	cgg Arg	acc Thr 255	cct Pro	gag Glu	gtc val	aca Thr	tgc Cys 260	gtg val	gtg	gtg	gac Asp	gtg Val 265	agc Ser	cac His	gaa Glu	gac Asp	864
	cct Pro 270	gag	gtc Val	aag Lys	ttc Phe	aac Asn 275	tgg Trp	tac Tyr	gtg Val	gac Asp	ggc Gly 280	gtg	gag Glu	gtg Val	cat His	aat Asn 285	912
	gcc	aag Lys	aca Thr	aag Lys	ccg Pro 290	cgg	gag Glu	gag Glu	cag Gln	tac Tyr 295	aac	agc Ser	acg Thr	tac Tyr	cgg Arg 300	gtg	960
					acc		ctg Leu			gac							1008
	tac Tyr	aag Lys	tgc Cys 320	aag	gtc Val	tcc Ser	aac Asn	aaa Lys 325	gcc Ala	ctc Leu	cca Pro	gcc Ala	ccc Pro 330	atc Ile	gag Glu	aaa Lys	1056
	acc Thr	atc Ile 335	tcc	aaa Lys	gcc Ala	aaa Lys	ggg Gly 340	cag	ccc Pro	cga Arg	gaa Glu	cca Pro 345	cag Gln	gtg Val	tac Tyr	acc Thr	1104
	ctg Leu 350	ccc	cca Pro	tcc Ser	cgg Arg	gat Asp 355	gag Glu	ctg Leu	acc Thr	aag Lys	aac Asn 360	cag Gln	gtc Val	agc Ser	ctg Leu	acc Thr 365	1152
	tgc	ctg Leu	gtc Val	aaa Lys	ggc Gly 370	ttc	tat Tyr	ccc Pro	agc Ser	gac Asp 375	atc Ile	gcc Ala	gtg val	gag Glu	tgg Trp 380	gag Glu	1200
	agc Ser	aat Asn	ggg Gly	cag Gln 385	ccg Pro	gag Glu	aac Asn	aac Asn	tac Tyr 390	aag Lys	acc Thr	acg Thr	cct Pro	ccc Pro 395	gtg Val	ctg Leu	1248
	gac Asp	tcc Ser	gac Asp 400	ggc Gly	tcc Ser	ttc Phe	ttc Phe	ctc Leu 405	tac Tyr	agc Ser	aag Lys	ctc Leu	acc Thr 410	gtg Val	gac Asp	aag Lys	1296
	agc Ser	agg Arg 415	tgg Trp	cag Gln	cag Gln	ggg Gly	aac Asn 420	gtc Val	ttc Phe	tca Ser	tgc Cys	tcc Ser 425	gtg Val	atg Met	cat His	gag Glu	1344
	gct Ala 430	ctg Leu	cac His	aac Asn	cac His	tac Tyr 435	acg Thr	cag Gln	aag Lys	agc Ser	ctc Leu 440	tcc Ser	ctg Leu	tct Ser	ccg Pro	ggt Gly 445	1392
	aaa Lys	tga															1398
<210> <211> <212> <213>	465 PRT	sap	oiens	5													
<400>	4	47-	-	V-1	C - 10	la .a			nh a		Not	475	415	۸٦۵	c1n	Con	
			-		-15		Leu			-10					-5		
			-1	1			Leu	5					10		_		
		15				-	Ile 20		-	_		25					
	30	-	-	_		35	Trp				40					45	
	Lys	Trp	Met	Gly	Trp 50	Ile	Asn	Thr	Tyr	Thr 55	Glu	Glu	Pro	Thr	Tyr 60	Gly	•
	Asp	Asp	Phe	Lys 65	Gly	Arg	Phe	Ala	Phe 70	Ser	Leu	Glu	Thr	Ser 75	Ala	Ser	
	Thr	Ala	Asn 80	Leu	Gln	Ile	Asn	Asn 85	Leu	Lys	Ser	Glu	Asp 90	Thr	Ala	Thr	
	Tyr	Phe	Cys	Ala	Arg	Phe	Gly 100	Ser	Ala	val	Asp	Tyr 105	Trp	Gly	Gln	Gly	
	Thr 110	Ser	۷a٦	Thr	٧a٦	Ser 115	Ser	Ala		Thr ne 4	Lys 120	Ġĺÿ	Pro	Ser	۷al	Phe 125	

Page 4

```
Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala Leu
                       130
                                            135
      Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser Trp
                   145
                                        150
                                                              155
      Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val Leu
                                    165
               160
                                                         170
      Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro Ser
          175
                                180
                                                     185
      Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His Lys Pro
                           195
                                                 200
                                                                      205
      Ser Asn Thr Lys Val Asp Lys Arg Val Glu Pro Lys Ser Cys Asp Lys
                                                                  220
                       210
                                            215
      Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly Pro
                   225
                                        230
                                                              235
      Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser
240 245 250
      Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His Glu Asp 255 260 265
      Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn
                           275
                                                280
      Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val
                       290
                                            295
                                                                  30Õ
      Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu
                   305
                                        310
                                                              315
         Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys 320 325 330
      Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr
                                340
                                                     345
      Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser Leu Thr 350 365 360 365
                           355
      Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu
370 375 380
      Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu 385 390 395
      Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys
              400
                                   405
                                                         410
      Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu
          415
                                                     425
                               420
      Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly
                           435
      430
                                                 440
      Lys
<210> 5
<211> 720
<212> DNA
<213> Homo sapiens
<220>
<221> misc_feature
<223> Low Risk Human Engineered ING-1 Light Chain (LC)
<220>
<221> misc_feature
<223> Variable Region of the Light Chain is Amino Acids 1-112
<220>
<221> CDS
<222> (1)..(717)
<220>
<221> mat_peptide
<222> (61)..()
```

<400>	г		٠.						NS	.txt							
· <400>	atg	agg Arg	ttc Phe	tct Ser	gct' Ala	Gln	ctt Leu	ctg Leu	ggg Gly	ctg Leu	ctt Leu -10	gtg Val	ctc Leu	tgg Trp	atc Ile	cct Pro -5	48
	gga	tcc Ser	act Thr	gca Ala -1	gac Asp	-15 atc Ile	gtg Val	atg Met	acc Thr	cag Gln	tct	gca Ala	ctc Leu	tcc Ser 10	aat Asn	cca	96
	gtc Val	act Thr	ctg Leu	gga	gag Glu	tca Ser	ggt Gly	tcc Ser	atc Ile	tcc Ser	tgc Cys	cgg Arg	tct Ser	agt	aag Lys	agt Ser	144
								act Thr									192
	cca Pro 45	ggg	cag Gln	tct Ser	cct Pro	Gln	ctg Leu	ctc Leu	atc Ile	tat Tyr	cag Gln	atg	tct Ser	aac Asn	aga Arg	gcc Ala 60	240
	tca	ggg Gly	gtc Val	cca Pro	Asp	50 agg Arg	ttc Phe	agt Ser	agc Ser	agt Ser	gga Gly	tct Ser	ggg Gly	aca Thr	Asp	ttc	288
	act Thr	ctc Leu	aag Lys	Ile	65 agc Ser	aga Arg	gtg Val	gag Glu	Ala	gaa Glu	gat Asp	gtg Val	gga Gly	gtt Val	75 tat Tyr	tac Tyr	336
								ccg Pro 100									384
	ctt Leu	gag Glu 110	atg	aaa Lys	cga Arg	act Thr	gtg Val 115	gct Ala	gca Ala	cca Pro	tct Ser	gtc Val 120	ttc Phe	atc Ile	ttc Phe	ccg Pro	432
	cca Pro 125	tct	gat Asp	gag Glu	cag Gln	ttg Leu 130	aaa	tct Ser	gga Gly	act Thr	gcc Ala 135	tct	gtt Val	gtg Val	tgc Cys	ctg Leu 140	480
	ctg					CCC		gag Glu			gta					gat	528
	aac Asn	gcc Ala	ctc Leu	caa Gln 160	tcg	ggt Gly	aac Asn	tcc Ser	cag Gln 165	gag	agt Ser	gtc Val	aca Thr	gag Glu 170	cag	gac Asp	576
	agc Ser	aag Lys	gac Asp 175	agc	acc Thr	tac Tyr	agc Ser	ctc Leu 180	agc	agc Ser	acc Thr	ctg Leu	acg Thr 185	ctg	agc Ser	aaa Lys	624
			tac					gtc Val					gtc				672
		ctg					aca	aag Lys				agg				tag	720
<210> <211> <212> <213>	239 PRT	sap	oiens	5													
<400>	Met	Arg	Phe	Ser	Аlа		Leu	Leu	Gly	Leu		۷al	Leu	Trp	Ile		
	-20 Gly	Ser	Thr	_	Asp	-15 Ile	٧a٦	Met	Thr	Gln	-10 Ser	Ala	Leu		Asn	-5 Pro	
	۷al	Thr		-1 Gly	G]u	Ser	Gly	Ser	Ile	Ser	Cys	Arg		10 Ser	Lys	Ser	
	Leu		His	Ser	Asn	Glу		Thr	Tyr	Leu	Tyr		25 Tyr	Leu	Gln	Lys	
	Pro 45	30 Gly	Gln	Ser	Pro	G]n 50	35 Leu	Leu	IJе	Tyr	G]n 55	40 Met	Ser	Asn	Arg	Ala 60	
	73					70			Pag	je 6	,,					50	

```
NS.txt
      Ser Gly Val Pro Asp Arg Phe Ser Ser Ser Gly Ser Gly Thr Asp Phe
                      65
                                           70
      Thr Leu Lys Ile Ser Arg Val Glu Ala Glu Asp Val Gly Val Tyr Tyr
                                       85
      Cys Ala Gln Asn Leu Glu Leu Pro Arg Thr Phe Gly Gln Gly Thr Lys
              95
                                                        105
                                   100
      Leu Glu Met Lys Arg Thr Val Ala Ala Pro Ser Val Phe Ile Phe Pro
                               115
      Pro Ser Asp Glu Gln Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu
                          130
                                               135
      125
      Leu Asn Asn Phe Tyr Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp
                      145
                                           150
                                                                155
      Asn Ala Leu Gln Ser Gly Asn Ser Gln Glu Ser Val Thr Glu Gln Asp
                  160
                                       165
                                                            170
      Ser Lys Asp Ser Thr Tyr Ser Leu Ser Ser Thr Leu Thr Leu Ser Lys
              175
                                   180
                                                       185
      Ala Asp Tyr Glu Lys His Lys Val Tyr Ala Cys Glu Val Thr His Gln 190 _ 195 200
      Gly Leu Ser Ser Pro Val Thr Lys Ser Phe Asn Arg Gly Glu Cys
                          210
<210> 7
<211> 720
<212> DNA
<213> Homo sapiens
<220>
<221> misc_feature
<223> Low + Moderate Risk Human Engineered ING-1 Light Chain (LC)
<220>
<221> CDS
<222> (1)..(717)
<220>
<221> mat_peptide
<222> (61) . ()
<400> 7
                                                                              48
      atg agg ttc tct gct cag ctt ctg ggg ctg ctt gtg ctc tgg atc cct
      Met Arg Phe Ser Ala Gln Leu Leu Gly Leu Leu Val Leu Trp Ile Pro
      -20
                                               -10
                                                                              96
      gga tcc act gca gac atc gtg atg acc cag tct cca ctc tcc ctg cca
      ĞÎy Ser Thr Ăla Ăsp Ile Vaî Met Thr Gln Ser Pro Leu Ser Leu Pro
                  -1 1
      gtc act cct gga gag ccg ggt tcc atc tcc tgc cgg tct agt aag agt
                                                                             144
      Val Thr Pro Gly Glu Pro Gly Ser Ile Ser Cys Arg Ser Ser Lys Ser
                                   20
              15
                                                       25
                                                                             192
      ctc cta cat agt aat ggc atc act tat ttg tat tgg tat ctg cag aaa
      Leu Leu His Ser Asn Gly Ile Thr Tyr Leu Tyr Trp Tyr Leu Gln Lys
          30
                              35
                                                   40
                                                                             240
      cca ggg cag tct cct cag ctg ctc atc tat cag atg tct aac aga gcc
      Pro ĞΟ GÎŇ Ser Pro GÎÑ Leŭ Leu Ile Tyr GÎÑ Met Ser Asn Arg Ala
      45
                          50
                                                                             288
      tca ggg gtc cca gac agg ttc agt agc agt gga tct ggg aca gat ttc
      Ser Gly Val Pro Asp Arg Phe Ser Ser Ser Gly Ser Gly Thr Asp Phe
                      65
                                                                             336
      act ctc aag atc agc aga gtg gag gct gaa gat gtg gga gtt tat tac
      Thr Leu Lys Ile Ser Arg Val Glū Āla Glu Āsp Val Gly Val Tyr Tyr
                                                                             384
      tgt gct cag aac cta gag ctt cca cgg acg ttc ggt cag ggc acc aag
      Cỷs Ăla Glň Asn Leu Glu Leu Pro Arg Thr Phe Gly Gln Gly Thr Lys
              95
                                                       105
                                   100
                                        Page 7
```

```
ctt gag atg aaa cga act gtg gct gca cca tct gtc ttc atc ttc ccg
Leu Glu Met Lys Arg Thr Val Ala Ala Pro Ser Val Phe Ile Phe Pro
                                                                                           432
                                    115
           110
                                                            120
       cca tct gat gag cag ttg aaa tct gga act gcc tct gtt gtg tgc ctg
Pro Ser Asp Glu Gln Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu
                                                                                           480
                               130
                                                       135
                                                                                140
       ctg aat aac ttc tat ccc aga gag gcc aaa gta cag tgg aag gtg gat
                                                                                           528
       Leu Asn Asn Phe Tyr Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp
                                                                                           576
       aac gcc ctc caa tcg ggt aac tcc cag gag agt gtc aca gag cag gac
Asn Ala Leu Gln Ser Gly Asn Ser Gln Glu Ser Val Thr Glu Gln Asp
                                              165
       agc aag gac agc acc tac agc ctc agc agc acc ctg acg ctg agc aaa
Ser Lys Asp Ser Thr Tyr Ser Leu Ser Ser Thr Leu Thr Leu Ser Lys
                                                                                           624
                175
                                         180
                                                                 185
       gca gac tac gag aaa cac aaa gtc tac gcc tgc gaa gtc acc cat cag
                                                                                           672
       Āla Āsp Tyr Glū Lys His Lys Val Tyr Āla Cys Ğlu Val Thr His Glñ
                                    195
                                                            200
       ggc ctg agc tcg ccc gtc aca aag agc ttc aac agg gga gag tgt tag
Gly Leu Ser Ser Pro Val Thr Lys Ser Phe Asn Arg Gly Glu Cys
                                                                                           720
                               210
                                                       215
<210> 8
<211> 239
<212> PRT
<213> Homo sapiens
<400> 8
       Met Arg Phe Ser Ala Gln Leu Leu Gly Leu Leu Val Leu Trp Ile Pro
                               -15
                                                       -10
       Gly Ser Thr Ala Asp Ile Val Met Thr Gln Ser Pro Leu Ser Leu Pro
                    -1 1
                                                                      10
       Val Thr Pro Gly Glu Pro Gly Ser Ile Ser Cys Arg Ser Ser Lys Ser
15 20 25
                15
       Leu Leu His Ser Asn Gly Ile Thr Tyr Leu Tyr Trp Tyr Leu Gln Lys
30 35 40
           30
                                    35
       Pro Gly Gln Ser Pro Gln Leu Leu Ile Tyr Gln Met Ser Asn Arg Ala
                               50
                                                       55
       Ser Gly Val Pro Asp Arg Phe Ser Ser Ser Gly Ser Gly Thr Asp Phe
                                                  70
                          65
       Thr Leu Lys Ile Ser Arg Val Glu Ala Glu Asp Val Gly Val Tyr Tyr
                                              85
       Cys Ala Gln Asn Leu Glu Leu Pro Arg Thr Phe Gly Gln Gly Thr Lys
                                                                 105
                                         100
                95
       Leu Glu Met Lys Arg Thr Val Ala Ala Pro Ser Val Phe Ile Phe Pro
                                    115
       Pro Ser Asp Glu Gln Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu
                               130
                                                       135
                                                                                140
       Leu Asn Asn Phe Tyr Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp
145 150 155
       Asn Ala Leu Gln Ser Gly Asn Ser Gln Glu Ser Val Thr Glu Gln Asp
                                                                      170
                     160
                                              165
       Ser Lys Asp Ser Thr Tyr Ser Leu Ser Ser Thr Leu Thr Leu Ser Lys
                175
                                        180
                                                                 185
       Ala Asp Tyr Glu Lys His Lys Val Tyr Ala Cys Glu Val Thr His Gln
                                    195
                                                           200
           190
       Gly Leu Ser Ser Pro Val Thr Lys Ser Phe Asn Arg Gly Glu Cys
                               210
                                                       215
<210> 9
<211> 88
<212> DNA
<213> Homo sapiens
```

<220> <221> <223>	misc_feature KL1 V Region Oligos Human Engineered ING-1 Light Chain (Kappa low)	
<400>	9 tgtcgacacc atgaggttct ctgctcagct tctggggctg cttgtgctct ggatccctgg atccactgca gacatcgtga tgacccag	60 88
<210> <211> <212> <213>	85	
	misc_feature KL2 V Region Oligos Human Engineered ING-1 Light Chain (Kappa low)	
<400>	10 actcttacta gaccggcagg agatggaacc tgactctccc agagtgactg gattggagag tgcagactgg gtcatcacga tgtct	60 85
<210> <211> <212> <213>	88	
	misc_feature KL3 V Region Oligos Human Engineered ING-1 Light Chain (Kappa low)	
<400>	11 ctgccggtct agtaagagtc tcctacatag taatggcatc acttatttgt attggtatct gcagaaacca gggcagtctc ctcagctg	60 88
<210> <211> <212> <213>	86	
<220> <221> <223>	misc_feature KL4 V Region Oligos Human Engineered ING-1 Light Chain (Kappa low)	
<400>	12 tgtcccagat ccactgctac tgaacctgtc tgggacccct gaggctctgt tagacatctg atagatgagc agctgaggag actgcc	60 86
<210> <211> <212> <213>	77	
<220> <221> <223>	misc_feature KL5 V Region Oligos Human Engineered ING-1 Light Chain (Kappa low)	
<400>	13 agcagtggat ctgggacaga tttcactctc aagatcagca gagtggaggc tgaagatgtg ggagtttatt actgtgc	60 77
<210>		

<212> <213>	DNA . Homo sapiens	
	misc_feature KL6 V Region Oligos Human Engineered ING-1 Light Chain (Kappa low)	
<400>	14 tttgatttca agcttggtgc cctgaccgaa cgtccgtgga agctctaggt tctgagcaca gtaataaact cccac	60 75
<210> <211> <212> <213>	22	
	misc_feature Low Risk Primers Forward Primer: KF ING-1 Light Chain Oligos	
<400>	15 ttatgtcgac accatgaggt tc	22
<210> <211> <212> <213>	21	
<220> <221> <223>	misc_feature Low risk Primers Reverse Primer: KR ING-1 Light Chain Oligos	
<400>	16 tttgatttca agcttggtgc c	21
<210> <211> <212> <213>	85	
<220> <221> <223>	misc_feature Moderate Risk Primer: KM2 V Region Oligos Human Engineered ING-1 Light Chain Oligos (Kappa Moderate)	
<400>	17 actcttacta gaccggcagg agatggaacc cggctctcca ggagtgactg gcagggagag tggagactgg gtcatcacga tgtct	60 85
<210> <211> <212> <213>	1398	
<220> <221> <223>	misc_feature Low Risk Human Engineered ING-1 Heavy Chain (HC)	
<220> <221> <223>	misc_feature Variable region of HC is Amino Acids is 1-116	
<220>		

```
<221> CDS
<222> (1)..(1395)
<220>
<221> mat_peptide
<222> (58)..()
<400> 18
        atg gct tgg gtg tcc acc ttg cta ttc ctg atg gca gct gcc caa agt
Met Ala Trp Val Ser Thr Leu Leu Phe Leu Met Ala Ala Ala Gln Ser
                                                                                                                 48
                                -15
                                                              -10
                                                                                            -5
        gcc caa gca cag atc cag ttg gtg cag tct gga cct gag gtg aag aag
Ala Gln Ala Gln Ile Gln Leu Val Gln Ser Gly Pro Glu Val Lys Lys
                                                                                                                96
                    -1 1
                                                                               10
        cct gga gag tcc gtc aag atc tcc tgc aag gct tct gga tat acc ttc
Pro Gly Glu Ser Val Lys Ile Ser Cys Lys Ala Ser Gly Tyr Thr Phe
                                                                                                               144
              15
                                            20
        aca aaa tat gga atg aac tgg gtg aag cag gct cca gga cag ggt tta
                                                                                                               192
        Thr Lys Tyr Gly Met Asn Trp Val Lys Gln Ala Pro Gly Gln Gly Leu
        aag tgg atg ggc tgg ata aac acc tac act gaa gag cca aca tat ggt
                                                                                                               240
        Lyš Trp̃ Met̃ Gly Trp̃ Ile Asn Thr Tyr Thr Glu Glu Pro Thr Tyr Gly
        gat gac ttc aag gga cgg ttt acc ttc acc ttg gac acc tct act agc Asp Asp Phe Lys Gly Arg Phe Thr Phe Thr Leu Asp Thr Ser Thr Ser
                                                                                                               288
                                                       70
                                                                                     75
        act gcc tat ttg gaa atc tct tct ctc cgg agt gag gac acg gct aca
                                                                                                               336
        Thr Ala Tyr Leu Glu Ile Ser Ser Leu Arg Ser Glu Asp Thr Ala Thr
                                                 85
                                                                               90
        tat ttc tgt gca aga ttt ggc tct gct gtg gac tac tgg ggt caa gga
Tyr Phe Cys Ala Arg Phe Gly Ser Ala Val Asp Tyr Trp Gly Gln Gly
                                                                                                               384
                                           100
                                                                         105
        acc ttg gtc acc gtc tcc tca gcc agc aca aag ggc cca tcg gtc ttc
Thr Leu Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val Phe
                                                                                                               432
                                     115
                                                                   120
        ccc ctg gca ccc tcc tcc aag agc acc tct ggg ggc aca gcg gcc ctg
Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala Leu
                                                                                                               480
                                130
                                                             135
        ggc tgc ctg gtc aag gac tac ttc ccc gaa ccg gtg acg gtg tcg tgg
Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser Trp
                                                                                                               528
                                                       150
        aac tca ggc gcc ctg acc agc ggc gtg cac acc ttc ccg gct gtc cta
Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val Leu
                                                                                                               576
                    160
                                                 165
                                                                               170
        cag tcc tca gga ctc tac tcc ctc agc agc gtg gtg acc gtg ccc tcc Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro Ser
                                                                                                               624
              175
                                           180
                                                                         185
        agc agc ttg ggc acc cag acc tac atc tgc aac gtg aat cac aag ccc
Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His Lys Pro
                                                                                                               672
                                     195
                                                                   200
                                                                                                 205
        agc aac acc aag gtg gac aag aga gtt gag ccc aaa tct tgt gac aaa
Ser Asn Thr Lys Val Asp Lys Arg Val Glu Pro Lys Ser Cys Asp Lys
                                                                                                               720
                               210
                                                             215
                                                                                                               768
        act cac aca tgc cca ccg tgc cca gca cct gaa ctc ctg ggg gga ccg
        Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly Pro
                                                       230
                                                                                                               816
        tca gtc ttc ctc ttc ccc cca aaa ccc aag gac acc ctc atg atc tcc
        Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser
                                                 245
        cgg acc cct gag gtc aca tgc gtg gtg gtg gac gtg agc cac gaa gac
Arg Thr Pro Glu Val Thr Cys Val Val Asp Val Ser His Glu Asp
                                                                                                               864
                                           260
                                                                         265
        cct gag gtc aag ttc aac tgg tac gtg gac ggc gtg gag gtg cat aat
                                                                                                               912
                                                        Page 11
```

```
NS.txt
      Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn
                             275
      270
                                                    280
                                                                            285
                                                                                      960
      gcc aag aca aag ccg cgg gag gag cag tac aac agc acg tac cgg gtg
      Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val
                                                295
                         290
                                                                                     1008
      gtc agc gtc ctc acc gtc ctg cac cag gac tgg ctg aat ggc aag gag
      Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu
                    305
                                            310
      tac aag tgc aag gtc tcc aac aaa gcc ctc cca gcc ccc atc gag aaa
Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys
                                                                                     1056
                320
                                       325
                                                              330
      acc atc tcc aaa gcc aaa ggg cag ccc cga gaa cca cag gtg tac acc
Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr
                                                                                     1104
                                  340
                                                         345
                                                                                     1152
      ctg ccc cca tcc cgg gat gag ctg acc aag aac cag gtc agc ctg acc
      Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser Leu Thr
      350
                             355
                                                     360
                                                                            365
      tgc ctg gtc aaa ggc ttc tat ccc agc gac atc gcc gtg gag tgg gag
Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu
                                                                                     1200
                         370
                                                375
      agc aat ggg cag ccg gag aac aac tac aag acc acg cct ccc gtg ctg
                                                                                     1248
      Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu
                                           390
                                                                   395
                    385
      gac tcc gac ggc tcc ttc ttc ctc tac agc aag ctc acc gtg gac aag
                                                                                     1296
      Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys
                                       405
                                                              410
      agc agg tgg cag cag ggg aac gtc ttc tca tgc tcc gtg atg cat gag
Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu
                                                                                     1344
                                  420
           415
                                                                                     1392
      gct ctg cac aac cac tac acg cag aag agc ctc tcc ctg tct ccg ggt
      Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly
                             435
                                                     440
      430
                                                                                     1398
      aaa tga
      Lys
<210> 19
<211> 465
<212> PRT
<213> Homo sapiens
<400> 19
      Met Ala Trp Val Ser Thr Leu Leu Phe Leu Met Ala Ala Ala Gln Ser
                                                -10
                         -15
      Ala Gln Ala Gln Ile Gln Leu Val Gln Ser Gly Pro Glu Val Lys Lys
               -1 1
      Pro Gly Glu Ser Val Lys Ile Ser Cys Lys Ala Ser Gly Tyr Thr Phe
                                  20
                                                         25
      Thr Lys Tyr Gly Met Asn Trp Val Lys Gln Ala Pro Gly Gln Gly Leu
                             35
                                                    40
      Lys Trp Met Gly Trp Ile Asn Thr Tyr Thr Glu Glu Pro Thr Tyr Gly
50 55 60
      Asp Asp Phe Lys Gly Arg Phe Thr Phe Thr Leu Asp Thr Ser Thr Ser 70 75
      Thr Ala Tyr Leu Glu Ile Ser Ser Leu Arg Ser Glu Asp Thr Ala Thr
                                      85
      Tyr Phe Cys Ala Arg Phe Gly Ser Ala Val Asp Tyr Trp Gly Gin Giy
                                                         105
                                  100
      Thr Leu Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val Phe
                             115
                                                    120
      Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala Leu
                         130
                                                135
      Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser Trp
```

150 Page 12

```
NS.txt
      Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val Leu
                                   165
                                                       170
              160
      Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro Ser
                              180
          175
                                                   185
      Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His Lys Pro
      190
                          195
                                               200
                                                                    205
      Ser Asn Thr Lys Val Asp Lys Arg Val Glu Pro Lys Ser Cys Asp Lys
                      210
                                           215
                                                                220
      Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly Pro
                  225
                                      230
                                                           235
      Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser
                                   245
      Arg Thr Pro Glu Val Thr Cys Val Val Asp Val Ser His Glu Asp
                               260
                                                   265
          255
      Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn
                          275
                                               280
      Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val
                                           295
                      290
                                                               300
      Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu
                                                           315
                                      310
                  305
      Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys
                                   325
                                                       330
              320
      Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr
          335
                              340
                                                   345
      Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser Leu Thr
                          355
                                               360
      Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu
                                           375
                      370
      Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu
                                                           395
                                       390
                  385
      Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys
              400
                                  405
                                                       410
      Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu
                              420
                                                   425
          415
      Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly
      430
                          435
                                               440
      Lys
<210> 20
<211> 1398
<212> DNA
<213> Homo sapiens
<220>
<221> misc_feature
<223> Low + Moderate Risk Human Engineered ING-1 Heavy Chain (HC)
<220>
<221> CDS
<222> (1)..(1395)
<220>
<221> mat_peptide
<222> (58)..()
<400> 20
                                                                              48
      atg gct tgg gtg tcc acc ttg cta ttc ctg atg gca gct gcc caa agt
     Met Ala Trp Val Ser Thr Leu Leu Phe Leu Met Ala Ala Ala Gln Ser
                                                                              96
      gcc caa gca cag atc cag ttg gtg cag tct gga gct gag gtg aag aag
     Ăla Gln Ăla Glň Ile Glň Leu Val Glň Ser Ğly Āla Ğlü Val Lys Lys
                                                       10
              -1 1
                                                                             144
      cct gga gag tca gtc aag atc tcc tgc aag gct tct gga tat acc ttc
                                       Page 13
```

٠								NC	++							
ro	Gly	Glu	Ser	٧a٦	Lys	Ile 20	Ser	Cys	.txt Lys	Ala	Ser 25	GΊу	Tyr	Thr	Phe	
aca Thr 30	aaa Lys	tat Tyr	gga Gly	atg Met	aac Asn 35	tgg	gtg Val	cga Arg	cag Gln	gct Ala 40	cca Pro	gga Gly	caa Gln	ggt Gly	tta Leu 45	192
gag	tgg Trp	atg Met	ggc Gly	tgg Trp 50	ata Ile	aac Asn	acc Thr	tac Tyr	act Thr 55	gaa	gag Glu	cca Pro	aca Thr	tat Tyr 60	ggt	240
cag Gln	aag Lys	ttc Phe	cag Gln 65	gga	cgg Arg	ttt Phe	acc Thr	ttc Phe 70	acc	ttg Leu	gac Asp	acc Thr	tct Ser 75	act Thr	agc Ser	288
act Thr	gcc Ala	tat Tyr 80	ttg	gaa Glu	atc Ile	tct Ser	tcg Ser 85	ctc Leu	cgg Arg	agt Ser	gag Glu	gac Asp 90	acg Thr	gct Ala	gtg Val	336
							tct	gct Ala								384
	ttg					tca		agc Ser			ggc					432
ccc	ctg Leu	gca Ala	ccc Pro	tcc Ser 130	tcc	aag Lys	agc Ser	acc Thr	tct Ser 135	ggg	ggc Gly	aca Thr	gcg Ala	gcc Ala 140	ctg	480
				aag				ccc Pro 150	gaa					tcg		528
aac Asn	tca Ser	ggc Gly 160	gcc	ctg Leu	acc Thr	agc Ser	ggc Gly 165	gtg Val	cac His	acc Thr	ttc Phe	ccg Pro 170	gct	gtc Val	cta Leu	576
cag Gln	tcc Ser 175	tca	gga Gly	ctc Leu	tac Tyr	tcc Ser 180	ctc Leu	agc Ser	agc Ser	gtg Val	gtg Val 185	acc Thr	gtg Val	ccc Pro	tcc Ser	624
								atc Ile								672
agc Ser	aac Asn	acc Thr	aag Lys	gtg Val 210	gac Asp	aag Lys	aga Arg	gtt Val	gag Glu 215	ccc Pro	aaa Lys	tct Ser	tgt Cys	gac Asp 220	aaa Lys	720
								gca Ala 230								768
			ctc					ccc Pro								816
cgg Arg	acc Thr 255	cct	gag Glu	gtc val	aca Thr	tgc Cys 260	gtg Val	gtg Val	gtg val	gac Asp	gtg Val 265	agc Ser	cac His	gaa Glu	gac Asp	864
cct Pro 270	gag	gtc Val	aag Lys	ttc Phe	aac Asn 275	tgg	tac Tyr	gtg Val	gac Asp	ggc Gly 280	gtg Val	gag Glu	gtg Val	cat His	aat Asn 285	912
gcc					cgg			cag Gln		aac						960
				acc				cag Gln 310								1008
tac Tyr	aag Lys	tgc Cys 320	aag	gtc Val	tcc Ser	aac Asn	aaa Lys 325	gcc Ala	ctc Leu	cca Pro	gcc Ala	ccc Pro 330	atc Ile	gag Glu	aaa Lys	1056
acc Thr	atc Ile 335	tcc Ser	aaa Lys	gcc Ala	aaa Lys	ggg Gly 340	cag Gln	ccc Pro	cga Arg	gaa Glu	cca Pro 345	cag Gln	gtg Val	tac Tyr	acc Thr	1104
ctg		cca	tcc	cgg	gat		ctg	acc Pag	aag e 14		-	gtc	agc	ctg	acc	1152

```
NS.txt
      Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser Leu Thr 350 365
      tgc ctg gtc aaa ggc ttc tat ccc agc gac atc gcc gtg gag tgg gag
                                                                                 1200
      Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu
                                             375
                                                                   380
                       370
      agc aat ggg cag ccg gag aac aac tac aag acc acg cct ccc gtg ctg
                                                                                 1248
      Sẽr Asn Gầy Glñ Pro Glù Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu
                                         390
      gac tcc gac ggc tcc ttc ttc ctc tac agc aag ctc acc gtg gac aag
Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys
                                                                                 1296
                                     405
                                                           410
      agc agg tgg cag ggg aac gtc ttc tca tgc tcc gtg atg cat gag
                                                                                 1344
      Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu
                                                      425
          415
                                420
      gct ctg cac aac cac tac acg cag aag agc ctc tcc ctg tct ccg ggt Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly
                                                                                 1392
      430
                            435
                                                  440
                                                                                 1398
      aaa tga
      Lys
<210> 21
<211> 465
<212> PRT
<213> Homo sapiens
      Met Ala Trp Val Ser Thr Leu Leu Phe Leu Met Ala Ala Ala Gln Ser
                       -15
                                             -10
      Ala Gln Ala Gln Ile Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys
              -1 1
      Pro Gly Glu Ser Val Lys Ile Ser Cys Lys Ala Ser Gly Tyr Thr Phe
15 20 25
          15
                                20
      Thr Lys Tyr Gly Met Asn Trp Val Arg Gln Ala Pro Gly Gln Gly Leu
                                                 40
      Glu Trp Met Gly Trp Ile Asn Thr Tyr Thr Glu Glu Pro Thr Tyr Gly
50 55 60
      Gln Lys Phe Gln Gly Arg Phe Thr Phe Thr Leu Asp Thr Ser Thr Ser
                                         70
      Thr Ala Tyr Leu Glu Ile Ser Ser Leu Arg Ser Glu Asp Thr Ala Val
              80
                                    85
      Tyr Phe Cys Ala Arg Phe Gly Ser Ala Val Asp Tyr Trp Gly Gln Gly
                                                      105
                                100
      Thr Leu Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val Phe
                            115
                                                  120
      Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala Leu
                                                                   140
                       130
                                             135
      Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser Trp
                                                               155
                   145
                                         150
      Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val Leu
                                    165
                                                          170
               160
      Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro Ser
          175
                                180
                                                      185
      Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His Lys Pro
                                                                        205
                            195
                                                 200
      Ser Asn Thr Lys Val Asp Lys Arg Val Glu Pro Lys Ser Cys Asp Lys
                                                                   220
                       210
                                             215
      Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly Pro
                                                               235
                   225
                                         230
      Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser
                                    245
                                                          250
               240
      Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His Glu Asp
                                260
                                                      265
      Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn
```

Page 15

```
275
                                                280
                                                                     285
      Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val
                       290
                                            295
                                                                300
      Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu
                  305
                                        310
      Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys
320 325 330
      Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr
                                                    345
          335
                               340
      Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser Leu Thr
                           355
                                                360
      350
                                                                     365
      Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu
                       370
                                            375
                                                                380
      Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu
                                       390
                                                            395
                   385
      Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys
              400
                                   405
                                                        410
      Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu
          415
                               420
                                                   425
      Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly
                           435
      430
                                                440
      Lys
<210> 22
<211> 91
<212> DNA
<213> Homo sapiens
<220>
<221> misc_feature
<223> GL1 V Region Oligos: Human Engineered ING-1 Heavy Chain Oligos
      (gamma low)
<400> 22
                                                                               60
      tgtcgacacc atggcttggg tgtccacctt gctattcctg atggcagctg cccaaagtgc
      ccaagcacag atccagttgg tgcagtctgg a
                                                                               91
<210> 23
<211> 90
<212> DNA
<213> Homo sapiens
<220>
<221> misc_feature
<223> GL2 V Region Oligos: Human Engineered ING-1 Heavy Chain Oligos
      (gamma low)
<400> 23
                                                                               60
      atattttgtg aaggtatatc cagaagcctt gcaggagatc ttgacggact ctccaggctt
      cttcacctca ggtccagact gcaccaactg
                                                                               90
<210> 24
<211> 91
<212> DNA
<213> Homo sapiens
<220>
<221> misc_feature
<223> GL3 V Region Oligos: Human Engineered ING-1 Heavy Chain Oligos
      (gamma low)
<400> 24
      tggatatacc ttcacaaaat atggaatgaa ctgggtgaag caggctccag gacagggttt
                                                                               60
                                        Page 16
```

	. NS.txt	
	aaagtggatg ggctggataa acacctacac t	91
<210> <211> <212> <213>	90	
	misc_feature GL4 V Region Oligos: Human Engineered ING-1 Heavy Chain Oligos (gamma low)	
<400>	25 cagtgctagt agaggtgtcc aaggtgaagg taaaccgtcc cttgaagtca tcaccatatg ttggctcttc agtgtaggtg tttatccagc	60 90
<210> <211> <212> <213>	90	
<220> <221> <223>	misc_feature GL5 V Region Oligos: Human Engineered ING-1 Heavy Chain Oligos (gamma low)	
<400>	26 gacacctcta ctagcactgc ctatttggaa atctcttctc tccggagtga ggacacggct acatattct gtgcaagatt tggctctgct	60 90
<210> <211> <212> <213>	85	
	misc_feature GL6 V Region Oligos: Human Engineered ING-1 Heavy Chain Oligos (gamma low)	
<400>	27 gaccgatggg ccctttgtgc tggctgagga gacggtgacc aaggttcctt gaccccagta gtccacagca gagccaaatc ttgca	60 85
<210> <211> <212> <213>	22	
<220> <221> <223>	misc_feature Human Engineered ING-1 Heavy Chain Oligos-Low Risk Primers Forward primer:GF	
<400>	28 ttatgtcgac accatggctt gg	22
<210> <211> <212> <213>	17	
<220>		

	misc_feature Human Engineered ING-1 Heavy Chain Oligos Low Risk Primers -Reverse Primer GR	
	misc_feature ING-1 Heavy Chain Oligos Low Risk Primers Reverse Primer GR	
<400>	29 gaccgatggg ccctttg	17
<210> <211> <212> <213>	90	
	misc_feature GM2 V Region Oligos Human Engineered ING-1 Heavy Chain Oligos-Low + Moderate Risk Primers	
<400>	30 atattttgtg aaggtatatc cagaagcctt gcaggagatc ttgactgact ctccaggctt cttcacctca gctccagact gcaccaactg	60 90
<210> <211> <212> <213>	91	
<220> <221> <223>	misc_feature GM3 V Region Oligos Human Engineered ING-1 Heavy Chain Oligos-Low + Moderate Risk Primers	
<400>	31 tggatatacc ttcacaaaat atggaatgaa ctgggtgcga caggctccag gacaaggttt agagtggatg ggctggataa acacctacac t	60 91
<210> <211> <212> <213>	90	
<220> <221> <223>	misc_feature GM4 V Region Oligos Human Engineered ING-1 Heavy Chain Oligos-Low + Moderate Risk Primers	
<400>	32 cagtgctagt agaggtgtcc aaggtgaagg taaaccgtcc ctggaacttc tgaccatatg ttggctcttc agtgtaggtg tttatccagc	60 90
<210> <211> <212> <213>	90	
<220> <221> <223>	misc_feature GM5 V Region Oligos Human Engineered ING-1 Heavy Chain Oligos-Low + Moderate Risk Primers	

```
<400> 33
        gacacctcta ctagcactgc ctatttggaa atctcttcgc tccggagtga ggacacggct
                                                                                                     60
        gtgtatttct gtgcaagatt tggctctgct
                                                                                                     90
<210> 34 ·
<211> 720
<212> DNA
<213> Homo sapiens
<220>
<221> misc_feature
<223> P1=P Human Engineered (low risk) ING1 light Chain with one
       moderate risk proline change; proline at position 8 (P1)
<220>
<221> CDS
<222> (1)..(717)
<220>
<221> mat_peptide
<222> (61)..()
<400> 34
        atg agg ttc tct gct cag ctt ctg ggg ctg ctt gtg ctc tgg atc cct
                                                                                                    48
       Met Arg Phe Ser Ala Glin Leu Leu Gly Leu Leu Val Leu Trp Ile Pro
                                  -15
                                                             -10
       gga tcc act gca gac atc gtg atg acc cag tct cca ctc tcc aat cca Gly Ser Thr Ala Asp Ile Val Met Thr Gln Ser Pro Leu Ser Asn Pro
                                                                                                    96
                        -1 1
       gtc act ctg gga gag tca ggt tcc atc tcc tgc cgg tct agt aag agt
Val Thr Leu Gly Glu Ser Gly Ser Ile Ser Cys Arg Ser Ser Lys Ser
                                                                                                   144
                                            20
                                                                       25
                  15
                                                                                                   192
        ctc cta cat agt aat ggc atc act tat ttg tat tgg tat ctg cag aaa
        Leu Leu His Ser Asn Gly Ile Thr Tyr Leu Tyr Trp Tyr Leu Gln Lys
                                        35
        cca ggg cag tct cct cag ctg ctc atc tat cag atg tct aac aga gcc
                                                                                                   240
        Pro GÍÝ GIM Ser Pro GIM Leu Leu Ile Tyr GIM Meť Ser Asn Arg Ála
                                  50
        tca ggg gtc cca gac agg ttc agt agc agt gga tct ggg aca gat ttc
                                                                                                   288
        Ser Gly Val Pro Asp Arg Phe Ser Ser Ser Gly Ser Gly Thr Asp Phe
       act ctc aag atc agc aga gtg gag gct gaa gat gtg gga gtt tat tac
Thr Leu Lys Ile Ser Arg Val Glu Ala Glu Asp Val Gly Val Tyr Tyr
                                                                                                   336
                                                  85
       tgt gct cag aac cta gag ctt ccg cgg acg ttc ggt cag ggc acc aag
Cys Ala Gln Asn Leu Glu Leu Pro Arg Thr Phe Gly Gln Gly Thr Lys
                                                                                                   384
                                            100
                                                                       105
       ctt gag atg aaa cga act gtg gct gca cca tct gtc ttc atc ttc ccg
Leu Glu Met Lys Arg Thr Val Ala Ala Pro Ser Val Phe Ile Phe Pro
                                                                                                   432
             110
                                       115
                                                                  120
       cca tct gat gag cag ttg aaa tct gga act gcc tct gtt gtg tgc ctg
Pro Ser Asp Glu Gln Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu
                                                                                                   480
                                  130
                                                            135
       ctg aat aac ttc tat ccc aga gag gcc aaa gta cag tgg aag gtg gat
                                                                                                   528
       Leu Asn Asn Phe Tyr Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp
                             145
       aac gcc ctc caa tcg ggt aac tcc cag gag agt gtc aca gag cag gac
Asn Ala Leu Gln Ser Gly Asn Ser Gln Glu Ser Val Thr Glu Gln Asp
                                                                                                   576
       agc aag gac agc acc tac agc ctc agc agc acc ctg acg ctg agc aaa
Ser Lys Asp Ser Thr Tyr Ser Leu Ser Ser Thr Leu Thr Leu Ser Lys
                                                                                                   624
                                            180
                                                                                                   672
       gca gac tac gag aaa cac aaa gtc tac gcc tgc gaa gtc acc cat cag
                                                  Page 19
```

```
NS.txt
      Ala Asp Tyr Glu Lys His Lys Val Tyr Ala Cys Glu Val Thr His Gln
          190
                              195
                                                    200
      ggc ctg agc tcg ccc gtc aca aag agc ttc aac agg gga gag tgt tag
                                                                              720
      Ğİy Leŭ Ser Ser Pro Val Thr Lys Ser Phe Asn Arg Ğİy Ğlü Cys
                          210
                                               215
<210> 35
<211> 239
<212> PRT
<213> Homo sapiens
<400> 35
      Met Arg Phe Ser Ala Gln Leu Leu Gly Leu Leu Val Leu Trp Ile Pro
                          -15
                                               -10
      Gly Ser Thr Ala Asp Ile Val Met Thr Gln Ser Pro Leu Ser Asn Pro
                                                            10
                  -1 1
      Val Thr Leu Gly Glu Ser Gly Ser Ile Ser Cys Arg Ser Ser Lys Ser 15 20 25
              15
      Leu Leu His Ser Asn Gly Ile Thr Tyr Leu Tyr Trp Tyr Leu Gln Lys
                               35
                                                   40
      Pro Gly Gln Ser Pro Gln Leu Leu Ile Tyr Gln Met Ser Asn Arg Ala
                          50
                                               55
      Ser Gly Val Pro Asp Arg Phe Ser Ser Ser Gly Ser Gly Thr Asp Phe
                      65
                                           70
      Thr Leu Lys Ile Ser Arg Val Glu Ala Glu Asp Val Gly Val Tyr Tyr
      Cys Ala Gln Asn Leu Glu Leu Pro Arg Thr Phe Gly Gln Gly Thr Lys
                                   100
                                                        105
      Leu Glu Met Lys Arg Thr Val Ala Ala Pro Ser Val Phe Ile Phe Pro
                              115
                                                   120
      Pro Ser Asp Glu Gln Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu
                          130
                                               135
      Leu Asn Asn Phe Tyr Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp
145 150 155
                                                                155
      Asn Ala Leu Gln Ser Gly Asn Ser Gln Glu Ser Val Thr Glu Gln Asp
                                       165
                                                            170
                  160
      Ser Lys Asp Ser Thr Tyr Ser Leu Ser Ser Thr Leu Thr Leu Ser Lys
              175
                                   180
      Ala Asp Tyr Glu Lys His Lys Val Tyr Ala Cys Glu Val Thr His Gln
                               195
          190
                                                   200
      Gly Leu Ser Ser Pro Val Thr Lys Ser Phe Asn Arg Gly Glu Cys
      205
                          210
                                               215
<210> 36
<211> 720
<212> DNA
<213> Homo sapiens
<220>
<221> misc_feature
<223> P2=P Human Engineered (low risk) ING1 light Chain with one
      moderate risk proline change; proline at position 15 (P2)
<220>
<221> CDS
<222> (1)..(717)
<220>
<221> mat_peptide
<222> (61)..()
<400> 36
                                                                               48
      atg agg ttc tct gct cag ctt ctg ggg ctg ctt gtg ctc tgg atc cct
                                       Page 20
```

									NC	+v+							
	Met -20	Arg	Phe	Ser	Ala	Gln -15	Leu	Leu		.txt Leu	Leu -10	٧al	Leu	Trp	Ile	Pro -5	
	gga Gly	tcc Ser	act Thr	gca Ala -1	gac Asp 1	atc Ile	gtg Val	atg Met	acc Thr 5	cag Gln	tct Ser	gca Ala	ctc Leu	tcc Ser 10	aat Asn	cca Pro	96
	gtc Val	act Thr	cct Pro 15	gga Gly	gag Glu	tca Ser	ggt Gly	tcc Ser 20	atc Ile	tcc Ser	tgc Cys	cgg Arg	tct Ser 25	agt Ser	aag Lys	agt Ser	144
			cat		aat Asn			act									192
	cca Pro 45	ggg	cag Gln	tct Ser	cct Pro	cag Gln 50	ctg Leu	ctc Leu	atc Ile	tat Tyr	cag Gln	atg Met	tct Ser	aac Asn	aga Arg	gcc Ala 60	240
	tca	ggg Gly	gtc Val	cca Pro	gac Asp	agg	ttc Phe	agt Ser	agc Ser	agt Ser 70	gga Gly	tct Ser	ggg Gly	aca Thr	gat Asp 75	ttc	288
	act Thr	ctc Leu	aag Lys	Ile	agc Ser	aga Arg	gtg val	gag Glu	Ala	gaa	gat Asp	gtg Val	gga Gly	gtt Val	tat	tac Tyr	336
	tgt Cys	gct Ala	Glñ	80 aac Asn	cta Leu	gag Glu	ctt Leu	ccg Pro 100	85 cgg Arg	acg Thr	ttc Phe	ggt Gly	Gln	ggc Gly	acc Thr	aag Lys	384
	ctt Leu	Glu	95 atg Met	aaa Lys	cga Arg	act Thr	val	gct	gca Ala	cca Pro	tct Ser	Val	105 ttc Phe	atc Ile	ttc Phe	ccg Pro	432
	Pro	110 tct Ser	gat Asp	gag Glu	cag Gln	Leu	115 aaa Lys	tct Ser	gga Gly	act Thr	gcc Ala 135	tct Ser	gtt Val	gtg Val	tgc Cys	ctg Leu 140	480
	125 ctg Leu	aat Asn	aac Asn	ttc Phe	tat Tyr 145	130 ccc Pro	aga Arg	gag Glu	gcc Ala	Lys	gta	cag Gln	tgg Trp	aag Lys	gtg Val 155	gat	528
	aac Asn	gcc Ala	ctc Leu	Gln	tcg Ser	ggt Gly	aac Asn	tcc Ser	Gln	gag Glu	agt Ser	gtc Val	aca Thr	gag Glu 170	cag	gac Asp	576
			Asp		acc Thr			Leu						ctg			624
	gca Ala	Ăsp	tac Tyr	gag Glu	aaa Lys	cac His	Lys	gtc Val	tac Tyr	gcc Ala	tgc Cys	gaa Glu 200	gtc	acc Thr	cat His	cag Gln	672
					ccc Pro		Thr					agg				tag	720
<210> <211> <212> <213>	239 PRT	sap	oiens	5													
<400>						_			_			_			_		
	Met -20	Arg	Phe	Ser	Ala	Gln -15	Leu	Leu	Gly	Leu	Leu -10	٧al	Leu	Trp	Ile	Pro -5	
	Gly	Ser	Thr	Ala -1	Asp 1	Ile	۷al	Met	Thr 5	Gln	Ser	Ala	Leu	Ser 10	Asn	Pro	
	٧a٦	Thr	Pro 15	бĪу	Ġlu	Ser	Gly	Ser 20	Ĭle	Ser	Cys	Arg	Ser 25		Lys	Ser	
	Leu			Ser	Asn	Gly	~ =	Thr	Tyr	Leu	Tyr	40		Leu	Gln	Lys	
		Gly	Gln	Ser	Pro	_ ~	35 Leu	Leu	IJе	Tyr	G]n	40 Met	Ser	Asn	Arg		
	45 Ser	Glу	٧a٦	Pro	Asp	50 Arg	Phe	Ser	Ser		Gly	Ser	Gly	Thr		60 Phe	
					65				Pag	70 e 21					/5		

```
NS.txt
      Thr Leu Lys Ile Ser Arg Val Glu Ala Glu Asp Val Gly Val Tyr Tyr
                                                                  90
      Cys Ala Gln Asn Leu Glu Leu Pro Arg Thr Phe Gly Gln Gly Thr Lys
                                      100
                                                             105
      Leu Glu Met Lys Arg Thr Val Ala Ala Pro Ser Val Phe Ile Phe Pro
                                  115
                                                         120
      Pro Ser Asp Glu Gln Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu
                                                                           140
                             130
                                                    135
      Leu Asn Asn Phe Tyr Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp
                         145
                                               150
                                                                      155
      Asn Ala Leu Gln Ser Gly Asn Ser Gln Glu Ser Val Thr Glu Gln Asp
                                           165
      Ser Lys Asp Ser Thr Tyr Ser Leu Ser Ser Thr Leu Thr Leu Ser Lys
               175
                                      180
                                                             185
      Ala Asp Tyr Glu Lys His Lys Val Tyr Ala Cys Glu Val Thr His Gln
_ 190 ____ 195 ____ 200
      Gly Leu Ser Ser Pro Val Thr Lys Ser Phe Asn Arg Gly Glu Cys
      205
                             210
<210> 38
<211> 720
<212> DNA
<213> Homo sapiens
<221> misc_feature
<223> P3=P Human Engineered (low risk) ING1 light Chain with one
      moderate risk proline change; proline at position 18 (P3)
<221> CDS
<222> (1)..(717)
<221> mat_peptide
<222> (61)..()
<400> 38
      atg agg ttc tct gct cag ctt ctg ggg ctg ctt gtg ctc tgg atc cct
                                                                                      48
      Met Arg Phe Ser Ala Gln Leu Leu Gly Leu Leu Val Leu Trp Ile Pro
      gga tcc act gca gac atc gtg atg acc cag tct gca ctc tcc aat cca
Gly Ser Thr Ala Asp Ile Val Met Thr Gln Ser Ala Leu Ser Asn Pro
                                                                                      96
                    -1 1
      gtc act ctg gga gag ccg ggt tcc atc tcc tgc cgg tct agt aag agt
                                                                                     144
      Val Thr Leu Gly Glu Pro Gly Ser Ile Ser Cys Arg Ser Ser Lys Ser
                                      20
                                                             25
               15
                                                                                     192
      ctc cta cat agt aat ggc atc act tat ttg tat tgg tat ctg cag aaa
      Leu Leu His Ser Asn Gly Ile Thr Tyr Leu Tyr Trp Tyr Leu Gln Lys
                                                         40
      cca ggg cag tct cct cag ctg ctc atc tat cag atg tct aac aga gcc
Pro Gly Gln Ser Pro Gln Leu Leu Ile Tyr Gln Met Ser Asn Arg Ala
                                                                                     240
      45
                             50
                                                    55
                                                                                     288
      tca ggg gtc cca gac agg ttc agt agc agt gga tct ggg aca gat ttc
      Ser Gly Val Pro Asp Arg Phe Ser Ser Ser Gly Ser Gly Thr Asp Phe
                                                                                     336
      act ctc aag atc agc aga gtg gag gct gaa gat gtg gga gtt tat tac
      Thr Leu Lyš Ile Ser Arg Val Glu Ala Glu Asp Val Gly Val Tyr Tyr
      tgt gct cag aac cta gag ctt ccg cgg acg ttc ggt cag ggc acc aag
Cys Ala Gln Asn Leu Glu Leu Pro Arg Thr Phe Gly Gln Gly Thr Lys
                                                                                     384
                                      100
                                                             105
                                                                                     432
      ctt gag atg aaa cga act gtg gct gca cca tct gtc ttc atc ttc ccg
                                           Page 22
```

<220>

<220>

<220>

```
NS.txt
      Leu Glu Met Lys Arg Thr Val Ala Ala Pro Ser Val Phe Ile Phe Pro
                                 115
                                                       120
           110
                                                                                   480
      cca tct gat gag cag ttg aaa tct gga act gcc tct gtt gtg tgc ctg
      Pro Ser Asp Glu Gln Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu
                                                   135
                            130
                                                                                   528
      ctg aat aac ttc tat ccc aga gag gcc aaa gta cag tgg aag gtg gat
      Leu Asn Asn Phe Tyr Pro Arg Glu Ala Lys Val Gln Trp Lys
                                                                   Val Asp
                                              150
                                                                    155
      aac gcc ctc caa tcg ggt aac tcc cag gag agt gtc aca gag cag gac
                                                                                   576
      Asn Ala Leu Gln Ser Gly Asn Ser Gln Glu Ser Val Thr Glu Gln Asp
                                          165
      agc aag gac agc acc tac agc ctc agc agc acc ctg acg ctg agc aaa
                                                                                   624
      Ser Lys Asp Ser Thr Tyr Ser Leu Ser Ser Thr Leu Thr Leu Ser Lys
               175
                                     180
                                                           185
      gca gac tac gag aaa cac aaa gtc tac gcc tgc gaa gtc acc cat cag
Ala Asp Tyr Glu Lys His Lys Val Tyr Ala Cys Glu Val Thr His Gln
                                                                                   672
                                 195
           190
                                                       200
      ggc ctg agc tcg ccc gtc aca aag agc ttc aac agg gga gag tgt tag
Gly Leu Ser Ser Pro Val Thr Lys Ser Phe Asn Arg Gly Glu Cys
                                                                                   720
                            210
<210> 39
<211> 239
<212> PRT
<213> Homo sapiens
<400> 39
      Met Arg Phe Ser Ala Gln Leu Leu Gly Leu Leu Val Leu Trp Ile Pro
                            -15
                                                  -10
      Gly Ser Thr Ala Asp Ile Val Met Thr Gln Ser Ala Leu Ser Asn Pro
                                                                10
                   -1 1
      Val Thr Leu Gly Glu Pro Gly Ser Ile Ser Cys Arg Ser Ser Lys Ser
15 20 25
      Leu Leu His Ser Asn Gly Ile Thr Tyr Leu Tyr Trp Tyr Leu Gln Lys 30 35 40
      Pro Gly Gln Ser Pro Gln Leu Leu Ile Tyr Gln Met Ser Asn Arg Ala
                            50
      Ser Gly Val Pro Asp Arg Phe Ser Ser Ser Gly Ser Gly Thr Asp Phe
                        65
                                              70
      Thr Leu Lys Ile Ser Arg Val Glu Ala Glu Asp Val Gly Val Tyr Tyr
      Cys Ala Gln Asn Leu Glu Leu Pro Arg Thr Phe Gly Gln Gly Thr Lys
               95
                                     100
                                                           105
      Leu Glu Met Lys Arg Thr Val Ala Ala Pro Ser Val Phe Ile Phe Pro
                                 115
                                                       120
      Pro Ser Asp Glu Gln Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu
                            130
                                                  135
                                                                         140
      Leu Asn Asn Phe Tyr Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp
145 150 155
      Asn Ala Leu Gln Ser Gly Asn Ser Gln Glu Ser Val Thr Glu Gln Asp
                                                               170
                   160
                                         165
      Ser Lys Asp Ser Thr Tyr Ser Leu Ser Ser Thr Leu Thr Leu Ser Lys
               175
                                     180
      Ala Asp Tyr Glu Lys His Lys Val Tyr Ala Cys Glu Val Thr His Gln
                                 195
          190
                                                       200
      Gly Leu Ser Ser Pro Val Thr Lys Ser Phe Asn Arg Gly Glu Cys
                            210
<210> 40
<211> 720
<212> DNA
<213> Homo sapiens
```

```
<220>
<221> misc_feature
<223> P1P2=Human Engineered (low risk) ING1 light Chain with one
       moderate risk proline change; proline at position 8 (P1) 15(P2)
<220>
<221> CDS
<222> (1)..(717)
<220>
<221> mat_peptide
<222> (61)..()
<400> 40
       atg agg ttc tct gct cag ctt ctg ggg ctg ctt gtg ctc tgg atc cct
Met Arg Phe Ser Ala Gln Leu Leu Gly Leu Leu Val Leu Trp Ile Pro
                                                                                                   48
                                                           -10
        -20
                                  -15
        gga tcc act gca gac atc gtg atg acc cag tct cca ctc tcc aat cca
                                                                                                   96
        Gly Ser Thr Ala Asp Ile Val Met Thr Gln Ser Pro Leu Ser Asn Pro
       gtc act cct gga gag tca ggt tcc atc tcc tgc cgg tct agt aag agt
                                                                                                  144
        Val Thr Pro Ğly Ğlü Ser Ğly Ser Ile Ser Cys Arg Ser Ser Lys Ser
                  15
       ctc cta cat agt aat ggc atc act tat ttg tat tgg tat ctg cag aaa
Leu Leu His Ser Asn Gly Ile Thr Tyr Leu Tyr Trp Tyr Leu Gln Lys
                                                                                                  192
       cca ggg cag tct cct cag ctg ctc atc tat cag atg tct aac aga gcc
                                                                                                  240
       Pro Gly Gln Ser Pro Gln Leu Leu Ile Tyr Gln Met Ser Asn Arg Ala
                                                            55
        45
                                  50
       tca ggg gtc cca gac agg ttc agt agc agt gga tct ggg aca gat ttc
Ser Gly Val Pro Asp Arg Phe Ser Ser Ser Gly Ser Gly Thr Asp Phe
                                                                                                  288
                            65
                                                      70
       act ctc aag atc agc aga gtg gag gct gaa gat gtg gga gtt tat tac
Thr Leu Lys Ile Ser Arg Val Glu Ala Glu Asp Val Gly Val Tyr Tyr
                                                                                                  336
                                                 85
                       80
                                                                                                  384
        tgt gct cag aac cta gag ctt ccg cgg acg ttc ggt cag ggc acc aag
       Cys Ala Gln Asn Leu Glu Leu Pro Arg Thr Phe Gly Gln Gly Thr Lys
                                                                      105
                                            100
       ctt gag atg aaa cga act gtg gct gca cca tct gtc ttc atc ttc ccg
Leu Glu Met Lys Arg Thr Val Ala Ala Pro Ser Val Phe Ile Phe Pro
                                                                                                  432
                                                                                                  480
        cca tct gat gag cag ttg aaa tct gga act gcc tct gtt gtg tgc ctg
        Pro Ser Ăsp Ğlü Glň Leŭ Lys Ser Ğİy Thr Ăla Ser Val Val Cys Leu
                                  130
                                                            135
                                                                                                  528
       ctg aat aac ttc tat ccc aga gag gcc aaa gta cag tgg aag gtg gat
Leu Asn Asn Phe Tyr Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp
                                                      150
                            145
                                                                                 155
       aac gcc ctc caa tcg ggt aac tcc cag gag agt gtc aca gag cag gac
Asn Ala Leu Gln Ser Gly Asn Ser Gln Glu Ser Val Thr Glu Gln Asp
                                                                                                  576
                                                                           170
                       160
                                                 165
                                                                                                  624
        agc aag gac agc acc tac agc ctc agc agc acc ctg acg ctg agc aaa
       Ser Lys Asp Ser Thr Tyr Ser Leu Ser Ser Thr Leu Thr Leu Ser Lys
                  175
                                            180
                                                                      185
                                                                                                  672
       gca gac tac gag aaa cac aaa gtc tac gcc tgc gaa gtc acc cat cag
       Ăla Āsp Tyr Ğlū Lys His Lys Val Tyr Āla Cys Glu Val Thr His Gln
                                       195
       ggc ctg agc tcg ccc gtc aca aag agc ttc aac agg gga gag tgt tag
Gly Leu Ser Ser Pro Val Thr Lys Ser Phe Asn Arg Gly Glu Cys
                                                                                                  720
                                  210
<210> 41
<211> 239
```

Page 24

<212> PRT

<213> Homo sapiens

```
<400> 41
      Met Arg Phe Ser Ala Gln Leu Leu Gly Leu Leu Val Leu Trp Ile Pro
                           -15
                                                -10
      Gly Ser Thr Ala Asp Ile Val Met Thr Gln Ser Pro Leu Ser Asn Pro
      Val Thr Pro Gly Glu Ser Gly Ser Ile Ser Cys Arg Ser Ser Lys Ser
                                   20
                                                        25 /
      Leu Leu His Ser Asn Gly Ile Thr Tyr Leu Tyr Trp Tyr Leu Gln Lys
                               35
      Pro Gly Gln Ser Pro Gln Leu Leu Ile Tyr Gln Met Ser Asn Arg Ala
                           50
      Ser Gly Val Pro Asp Arg Phe Ser Ser Ser Gly Ser Gly Thr Asp Phe
65 70 75
                      65
      Thr Leu Lys Ile Ser Arg Val Glu Ala Glu Asp Val Gly Val Tyr Tyr
      Cys Ala Gln Asn Leu Glu Leu Pro Arg Thr Phe Gly Gln Gly Thr Lys
                                   100
                                                        105
      Leu Glu Met Lys Arg Thr Val Ala Ala Pro Ser Val Phe Ile Phe Pro
                               115
      Pro Ser Asp Glu Gln Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu
                                                135
      125
                           130
      Leu Asn Asn Phe Tyr Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp
145 150 155
      Asn Ala Leu Gln Ser Gly Asn Ser Gln Glu Ser Val Thr Glu Gln Asp
                                       165
      Ser Lys Asp Ser Thr Tyr Ser Leu Ser Ser Thr Leu Thr Leu Ser Lys
                                   180
      Ala Asp Tyr Glu Lys His Lys Val Tyr Ala Cys Glu Val Thr His Gln
                               195
          190
                                                   200
      Gly Leu Ser Ser Pro Val Thr Lys Ser Phe Asn Arg Gly Glu Cys
      205
                           210
<210> 42
<211> 720
<212> DNA
<213> Homo sapiens
<220>
<221> misc_feature
<223> P1P3= Human Engineered (low risk) ING1 light Chain with one
      moderate risk proline change; proline at position 8 (P1) 18 (P3)
<220>
<221> CDS
<222> (1)..(717)
<220>
<221> mat_peptide
<222> (61)..()
<400> 42
                                                                              48
      atg agg ttc tct gct cag ctt ctg ggg ctg ctt gtg ctc tgg atc cct
      Met Arg Phe Ser Ala Glm Leu Leu Gly Leu Leu Val Leu Trp Ile Pro
      -20
                                                -10
                                                                              96
      gga tcc act gca gac atc gtg atg acc cag tct cca ctc tcc aat cca
      ĞÎy Ser Thr Āla Āsp Ile Val Met Thr Glñ Ser Pro Leu Ser Asn Pro
                                                                              144
      gtc act ctg gga gag ccg ggt tcc atc tcc tgc cgg tct agt aag agt
      Val Thr Leu Gly Glu Pro Gly Ser Ile Ser Cys Arg Ser Ser Lys Ser
                                   20
      ctc cta cat agt aat ggc atc act tat ttg tat tgg tat ctg cag aaa
                                                                              192
                                        Page 25
```

```
Leu Leu His Ser Asn Gly Ile Thr Tyr Leu Tyr Trp Tyr Leu Gln Lys
            30
                                    35
                                                             40
       cca ggg cag tct cct cag ctg ctc atc tat cag atg tct aac aga gcc
                                                                                            240
       Pro Gly Gln Ser Pro Gln Leu Leu Ile Tyr Gln Met Ser Asn Arg Ala
       45
       tca ggg gtc cca gac agg ttc agt agc agt gga tct ggg aca gat ttc
Ser Gly Val Pro Asp Arg Phe Ser Ser Ser Gly Ser Gly Thr Asp Phe
                                                                                            288
                                                   70
       act ctc aag atc agc aga gtg gag gct gaa gat gtg gga gtt tat tac
Thr Leu Lys Ile Ser Arg Val Glu Ala Glu Asp Val Gly Val Tyr Tyr
                                                                                            336
                                                                       90
                                              85
                                                                                            384
       tgt gct cag aac cta gag ctt ccg cgg acg ttc ggt cag ggc acc aag
       Cys Ala Gln Asn Leu Glu Leu Pro Arg Thr Phe Gly Gln Gly Thr Lys
                 95
                                         100
                                                                  105
       ctt gag atg aaa cga act gtg gct gca cca tct gtc ttc atc ttc ccg
Leu Glu Met Lys Arg Thr Val Ala Ala Pro Ser Val Phe Ile Phe Pro
                                                                                            432
                                                             120
                                    115
            110
       cca tct gat gag cag ttg aaa tct gga act gcc tct gtt gtg tgc ctg
                                                                                            480
       Pro Ser Asp Glu Gln Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu
                               130
                                                        135
       ctg aat aac ttc tat ccc aga gag gcc aaa gta cag tgg aag gtg gat
                                                                                            528
       Leu Asn Asn Phe Tyr Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp
       aac gcc ctc caa tcg ggt aac tcc cag gag agt gtc aca gag cag gac
Asn Ala Leu Gln Ser Gly Asn Ser Gln Glu Ser Val Thr Glu Gln Asp
                                                                                            576
                                              165
                                                                                            624
       agc aag gac agc acc tac agc ctc agc agc acc ctg acg ctg agc aaa
       Ser Lys Asp Ser Thr Tyr Ser Leu Ser Ser Thr Leu Thr Leu Ser Lys
                175
                                         180
                                                                  185
       gca gac tac gag aaa cac aaa gtc tac gcc tgc gaa gtc acc cat cag
Ala Asp Tyr Glu Lys His Lys Val Tyr Ala Cys Glu Val Thr His Gln
                                                                                            672
                                    195
           190
                                                             200
       ggc ctg agc tcg ccc gtc aca aag agc ttc aac agg gga gag tgt tag
Gly Leu Ser Ser Pro Val Thr Lys Ser Phe Asn Arg Gly Glu Cys
                                                                                            720
                               210
<210> 43
<211> 239
<212> PRT
<213> Homo sapiens
<400> 43
       Met Arg Phe Ser Ala Gln Leu Leu Gly Leu Leu Val Leu Trp Ile Pro
                                -15
                                                        -10
       Gly Ser Thr Ala Asp Ile Val Met Thr Gln Ser Pro Leu Ser Asn Pro
                                                                       10
                     -1 1
       Val Thr Leu Gly Glu Pro Gly Ser Ile Ser Cys Arg Ser Ser Lys Ser
15 20 25
       Leu Leu His Ser Asn Gly Ile Thr Tyr Leu Tyr Trp Tyr Leu Gln Lys
                                    35
                                                             40
       Pro Gly Gln Ser Pro Gln Leu Leu Ile Tyr Gln Met Ser Asn Arg Ala
                               50
       Ser Gly Val Pro Asp Arg Phe Ser Ser Ser Gly Ser Gly Thr Asp Phe
                                                   70
                          65
       Thr Leu Lys Ile Ser Arg Val Glu Ala Glu Asp Val Gly Val Tyr Tyr
                                              85
       Cys Ala Gln Asn Leu Glu Leu Pro Arg Thr Phe Gly Gln Gly Thr Lys
                                         100
                                                                  105
       Leu Glu Met Lys Arg Thr Val Ala Ala Pro Ser Val Phe Ile Phe Pro
                                    115
                                                             120
```

Pro Ser Asp Glu Gln Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu

Leu Asn Asn Phe Tyr Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp

Page 26

135

130

```
NS.txt
                                                  150
       Asn Ala Leu Gln Ser Gly Asn Ser Gln Glu Ser Val Thr Glu Gln Asp
                     160
                                             165
                                                                     170
       Ser Lys Asp Ser Thr Tyr Ser Leu Ser Ser Thr Leu Thr Leu Ser Lys
                175
                                        180
                                                                 185
       Ala Asp Tyr Glu Lys His Lys Val Tyr Ala Cys Glu Val Thr His Gln
                                    195
           190
                                                            200
       Gly Leu Ser Ser Pro Val Thr Lys Ser Phe Asn Arg Gly Glu Cys
                               210
<210> 44
<211> 720
<212> DNA
<213> Homo sapiens
<220>
<221> misc_feature
<223> P2P3=Human Engineered (low risk) ING1 light Chain with one
      moderate risk proline change; proline at position 8 (P1) 18 (P3)
<220>
<221> CDS
<222> (1)..(717)
<220>
<221> mat_peptide
<222> (61)..()
<400> 44
      atg agg ttc tct gct cag ctt ctg ggg ctg ctt gtg ctc tgg atc cct
Met Arg Phe Ser Ala Gln Leu Leu Gly Leu Leu Val Leu Trp Ile Pro
                                                                                           48
       -20
                               -15
                                                       -10
      gga tcc act gca gac atc gtg atg acc cag tct gca ctc tcc aat cca
Gly Ser Thr Ala Asp Ile Val Met Thr Gln Ser Ala Leu Ser Asn Pro
                                                                                           96
                     -1 1
       gtc act cct gga gag ccg ggt tcc atc tcc tgc cgg tct agt aag agt
                                                                                          144
       Val Thr Pro Gly Glu Pro Gly Ser Ile Ser Cys Arg Ser Ser Lys Ser
                                        20
       ctc cta cat agt aat ggc atc act tat ttg tat tgg tat ctg cag aaa
                                                                                          192
       Leu Leu His Ser Asn Gly Ile Thr Tyr Leu Tyr Trp Tyr Leu Gln Lys
                                                                                          240
       cca ggg cag tct cct cag ctg ctc atc tat cag atg tct aac aga gcc
       Pro Gly Gln Ser Pro Gln Leu Leu Ile Tyr Gln Met Ser Asn Arg Åla
       45
                               50
                                                                                          288
       tca ggg gtc cca gac agg ttc agt agc agt gga tct ggg aca gat ttc
       Ser Gly Val Pro Asp Arg Phe Ser Ser Ser Gly Ser Gly Thr Asp Phe
                         65
                                                  70
                                                                          75
      act ctc aag atc agc aga gtg gag gct gaa gat gtg gga gtt tat tac
Thr Leu Lys Ile Ser Arg Val Glu Ala Glu Asp Val Gly Val Tyr Tyr
                                                                                          336
                                             85
      tgt gct cag aac cta gag ctt ccg cgg acg ttc ggt cag ggc acc aag
Cys Ala Gln Asn Leu Glu Leu Pro Arg Thr Phe Gly Gln Gly Thr Lys
                                                                                          384
                                        100
                                                                                          432
       ctt gag atg aaa cga act gtg gct gca cca tct gtc ttc atc ttc ccg
       Leu Glū Met Lys Arg Thr Val Ala Ala Pro Ser Val Phe Ile Phe Pro
                                   112
      cca tct gat gag cag ttg aaa tct gga act gcc tct gtt gtg tgc ctg
Pro Ser Asp Glu Gln Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu
                                                                                          480
                               130
                                                                                          528
       ctg aat aac ttc tat ccc aga gag gcc aaa gta cag tgg aag gtg gat
      Leu Asn Asn Phe Tyr Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp
                                                  150
                                                                                          576
      aac gcc ctc caa tcg ggt aac tcc cag gag agt gtc aca gag cag gac
                                             Page 27
```

```
NS.txt
      Asn Ala Leu Gln Ser Gly Asn Ser Gln Glu Ser Val Thr Glu Gln Asp
                   160
                                        165
                                                              170
                                                                                624
      age aag gae age ace tae age etc age age ace etg aeg etg age aaa
      Ser Lys Asp Ser Thr Tyr Ser Leu Ser Ser Thr Leu Thr Leu Ser Lys
                                    180
      gca gac tac gag aaa cac aaa gtc tac gcc tgc gaa gtc acc cat cag
Ala Asp Tyr Glu Lys His Lys Val Tyr Ala Cys Glu Val Thr His Gln
                                                                                672
                                                     200
                                                                                720
      ggc ctg agc tcg ccc gtc aca aag agc ttc aac agg gga gag tgt tag
      Gly Leu Ser Ser Pro Val Thr Lys Ser Phe Asn Arg Gly Glu Cys
                            210
                                                 215
<210> 45
<211> 239
<212> PRT
<213> Homo sapiens
<400> 45
      Met Arg Phe Ser Ala Gln Leu Leu Gly Leu Leu Val Leu Trp Ile Pro
                                                 -10
      Gly Ser Thr Ala Asp Ile Val Met Thr Gln Ser Ala Leu Ser Asn Pro
                                                              10
                   -1 1
      Val Thr Pro Gly Glu Pro Gly Ser Ile Ser Cys Arg Ser Ser Lys Ser
                                    20
      Leu Leu His Ser Asn Gly Ile Thr Tyr Leu Tyr Trp Tyr Leu Gln Lys
                                                     40
          30
                                35
      Pro Gly Gln Ser Pro Gln Leu Leu Ile Tyr Gln Met Ser Asn Arg Ala
      Ser Gly Val Pro Asp Arg Phe Ser Ser Ser Gly Ser Gly Thr Asp Phe 65 70 75
                       65
      Thr Leu Lys Ile Ser Arg Val Glu Ala Glu Asp Val Gly Val Tyr Tyr
                                        85
      Cys Ala Gln Asn Leu Glu Leu Pro Arg Thr Phe Gly Gln Gly Thr Lys
                                    100
                                                         105
      Leu Glu Met Lys Arg Thr Val Ala Ala Pro Ser Val Phe Ile Phe Pro
          110
                                115
      Pro Ser Asp Glu Gln Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu
                                                 135
                           130
      Leu Asn Asn Phe Tyr Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp
145 150 155
      Asn Ala Leu Gln Ser Gly Asn Ser Gln Glu Ser Val Thr Glu Gln Asp
                                                              170
                                        165
      Ser Lys Asp Ser Thr Tyr Ser Leu Ser Ser Thr Leu Thr Leu Ser Lys
               175
                                    180
                                                          185
      Ala Asp Tyr Glu Lys His Lys Val Tyr Ala Cys Glu Val Thr His Gln
                                195
                                                     200
          190
      Gly Leu Ser Ser Pro Val Thr Lys Ser Phe Asn Arg Gly Glu Cys
      205
                            210
<210> 46
<211> 85
<212> DNA
<213> Homo sapiens
<220>
<221> misc_feature
<223> P1 Oligo Human Engineered ING-1 with proline oligos
<400> 46
      actcttacta gaccggcagg agatggaacc tgactctccc agagtgactg gattggagag
                                                                                 60
      tggagactgg gtcatcacga tgtct
                                                                                 85
<210> 47
```

<211>	NS. LAC	
<212>		
	misc_feature P2 Oligo Human Engineered ING-1 with proline oligos	
<400>	47 actcttacta gaccggcagg agatggaacc tgactctcca ggagtgactg gattggagag tgcagactgg gtcatcacga tgtct	60 85
<210> <211> <212> <213>	85	
<220> <221> <223>	misc_feature P3 Oligo Human Engineered ING-1 with proline oligos	
<400>	48 actcttacta gaccggcagg agatggaacc cggctctccc agagtgactg gattggagag tgcagactgg gtcatcacga tgtct	60 85
<210> <211> <212> <213>	85	•
<220> <221> <223>	misc_feature P1P2 Oligo Human Engineered ING-1 with proline oligos	
<400>	49 actcttacta gaccggcagg agatggaacc cggctctcca ggagtgactg gattggagag tgcagactgg gtcatcacga tgtct	60 85
<210> <211> <212> <213>	85	
	misc_feature P1P3 Oligo Human Engineered ING-1 with proline oligos	
<400>	50 actcttacta gaccggcagg agatggaacc cggctctccc agagtgactg gattggagag tggagactgg gtcatcacga tgtct	60 85
<210> <211> <212> <213>	85	
<220> <221> <223>	misc_feature P2P3 Oligo Human Engineered ING-1 with proline oligos	
<400>	51 actcttacta gaccggcagg agatggaacc cggctctcca ggagtgactg gattggagag tgcagactgg gtcatcacga tgtct Page 29	60 85

```
<210> 52
<211> 19
<212> DNA
<213> Homo sapiens
<220>
<221> misc_feature
<223> Reverse Primer KBsr ING-1 Light Chain
<400> 52
                                                                                                         19
        cttactagac cggcaggag
<210> 53
<211> 798
<212> DNA
<213> Homo sapiens
<220>
<221> misc_feature
<223> EpCam truncated sequence
<220>
<221> CDS
<222> (1)..(795)
<400> 53
        48
                                                         10
                                                                                     15
        acg gcg act ttt gcc gca gct cag gaa gaa tgt gtc tgt gaa aac tac
Thr Ala Thr Phe Ala Ala Ala Gln Glu Glu Cys Val Cys Glu Asn Tyr
                                                                                                         96
                                                    25
        aag ctg gcc gta aac tgc ttt gtg aat aat aat cgt caa tgc cag tgt
Lys Leu Ala Val Asn Cys Phe Val Asn Asn Asn Arg Gln Cys Gln Cys
                                                                                                        144
                   35
                                              40
        act tca gtt ggt gca caa aat act gtc att tgc tca aag ctg gct gcc
Thr Ser Val Gly Ala Gln Asn Thr Val Ile Cys Ser Lys Leu Ala Ala
                                                                                                        192
                                         55
        aaa tgt ttg gtg atg aag gca gaa atg aat ggc tca aaa ctt ggg aga
Lys Cys Leu Val Met Lys Ala Glu Met Asn Gly Ser Lys Leu Gly Arg
                                                                                                        240
        65
        aga gca aaa cct gaa ggg gcc ctc cag aac aat gat ggg ctt tat gat
Arg Ala Lys Pro Glu Gly Ala Leu Gln Asn Asn Asp Gly Leu Tyr Asp
                                                                                                        288
                              85
                                                         90
                                                                                                        336
        cct gac tgc gat gag agc ggg ctc ttt aag gcc aag cag tgc aac ggc
Pro Asp Cys Asp Glu Ser Gly Leu Phe Lys Ala Lys Gln Cys Asn Gly
                        100
                                                    105
        acc tcc acg tgc tgg tgt gtg aac act gct ggg gtc aga aga aca gac
Thr Ser Thr Cys Trp Cys Val Asn Thr Ala Gly Val Arg Arg Thr Asp
                                                                                                        384
                                              120
                                                                          125
                   115
        aag gac act gaa ata acc tgc tct gag cga gtg aga acc tac tgg atc
                                                                                                        432
        Lys Asp Thr Glu Ile Thr Cys Ser Glu Arg Val Arg Thr Tyr Trp Ile
                                         135
                                                                                                        480
        atc att gaa cta aaa cac aaa gca aga gaa aaa cct tat gat agt aaa
        Ile Ile Glu Leu Lys His Lys Ala Arg Glu Lys Pro Tyr Asp Ser Lys
145 150 155 160
        agt ttg cgg act gca ctt cag aag gag atc aca acg cgt tat caa ctg
Ser Leu Arg Thr Ala Leu Gln Lys Glu Ile Thr Thr Arg Tyr Gln Leu
                                                                                                        528
                                                         170
        gat cca aaa ttt atc acg agt att ttg tat gag aat aat gtt atc act
                                                                                                        576
        Asp Pro Lys Phe Ile Thr Ser Ile Leu Tyr Glu Asn Asn Val Ile Thr
                                                    185
                                                                                190
                                                     Page 30
```

```
att gat ctg gtt caa aat tct tct caa aaa act cag aat gat gtg gac
                                                                                             624
       Ile Asp Leu Val Gln Asn Ser Ser Gln Lys Thr Gln Asn Asp Val Asp
                                                                  205
                 195
                                         200
       ata gct gat gtg gct tat tat ttt gaa aaa gat gtt aaa ggt gaa tcc
Ile Ala Asp Val Ala Tyr Tyr Phe Glu Lys Asp Val Lys Gly Glu Ser
                                                                                             672
                                     215
            210
       ttg ttt cat tct aag aaa atg gac ctg aca gta aat ggg gaa caa ctg
Leu Phe His Ser Lys Lys Met Asp Leu Thr Val Asn Gly Glu Gln Leu
225 230 235 240
                                                                                            720
       gat ctg gat cct ggt caa act tta att tat tat gtt gat gaa aaa gca
Asp Leu Asp Pro Gly Gln Thr Leu Ile Tyr Tyr Val Asp Glu Lys Ala
                                                                                            768
                           245
                                                   250
       cct gaa ttc tca atg cag ggt cta aaa taa
Pro Glu Phe Ser Met Gln Gly Leu Lys
                                                                                            798
                      260
<210> 54
<211> 265
<212> PRT
<213> Homo sapiens
<400> 54
       Met Ala Pro Pro Gln Val Leu Ala Phe Gly Leu Leu Ala Ala Ala
       Thr Ala Thr Phe Ala Ala Ala Gln Glu Glu Cys Val Cys Glu Asn Tyr
                      20
                                              25
       Lys Leu Ala Val Asn Cys Phe Val Asn Asn Asn Arg Gln Cys Gln Cys 35 40 45
       Thr Ser Val Gly Ala Gln Asn Thr Val Ile Cys Ser Lys Leu Ala Ala 50 _ 60 _ 60 _
       Lys Cys Leu Val Met Lys Ala Glu Met Asn Gly Ser Lys Leu Gly Arg 65 70 75 80
       Arg Ala Lys Pro Glu Gly Ala Leu Gln Asn Asn Asp Gly Leu Tyr Asp 85 90 95
                          85
       Pro Asp Cys Asp Glu Ser Gly Leu Phe Lys Ala Lys Gln Cys Asn Gly 100 105 110
       Thr Ser Thr Cys Trp Cys Val Asn Thr Ala Gly Val Arg Arg Thr Asp
                                         120
                                                                  125
                115
       Lys Asp Thr Glu Ile Thr Cys Ser Glu Arg Val Arg Thr Tyr Trp Ile
130 135 140
            130
       Ile Ile Glu Leu Lys His Lys Ala Arg Glu Lys Pro Tyr Asp Ser Lys
145 150 155 160
       Ser Leu Arg Thr Ala Leu Gln Lys Glu Ile Thr Thr Arg Tyr Gln Leu
                           165
                                                   170
       Asp Pro Lys Phe Ile Thr Ser Ile Leu Tyr Glu Asn Asn Val Ile Thr
                                                                       190
                                              185
                     180
       Ile Asp Leu Val Gln Asn Ser Ser Gln Lys Thr Gln Asn Asp Val Asp
                                         200
                                                                  205
                195
       Ile Ala Asp Val Ala Tyr Tyr Phe Glu Lys Asp Val Lys Gly Glu Ser 210 220
       Leu Phe His Ser Lys Lys Met Asp Leu Thr Val Asn Gly Glu Gln Leu 225 230 235 240
       Asp Leu Asp Pro Gly Gln Thr Leu Ile Tyr Tyr Val Asp Glu Lys Ala
                                                   250
                          245
       Pro Glu Phe Ser Met Gln Gly Leu Lys
                      260
<210> 55
<211> 945
<212> DNA
<213> Homo sapiens
<220>
```

```
<221> misc_feature
<223> Full-Length EpCam
<220>
<221> CDS
<222> (1)..(942)
<220>
<221> mat_peptide
<222> (70)..()
<400> 55
       48
                                                 -15
                       -20
                                                                           -10
       acg gcg act ttt gcc gca gct cag gaa gaa tgt gtc tgt gaa aac tac
Thr Ala Thr Phe Ala Ala Ala Gln Glu Glu Cys Val Cys Glu Asn Tyr
                                                                                                   96
                                      -1 1
       aag ctg gcc gta aac tgc ttt gtg aat aat aat cgt caa tgc cag tgt
                                                                                                  144
       Lys Leu Ala Val Asn Cys Phe Val Asn Asn Asn Arg Gln Cys Gln Cys
                                                            20
                                                                                                  192
       act tca gtt ggt gca caa aat act gtc att tgc tca aag ctg gct gcc
       Thr Ser Val Gly Ala Gln Asn Thr Val Ile Cys Ser Lys Leu Ala Ala
       aaa tgt ttg gtg atg aag gca gaa atg aat ggc tca aaa ctt ggg aga
Lys Cys Leu Val Met Lys Ala Glu Met Asn Gly Ser Lys Leu Gly Arg
                                                                                                  240
                                                 50
       aga gca aaa cct gaa ggg gcc ctc cag aac aat gat ggg ctt tat gat
Arg Ala Lys Pro Glu Gly Ala Leu Gln Asn Asn Asp Gly Leu Tyr Asp
                                                                                                  288
                                                                      70
                 60
                                           65
       cct gac tgc gat gag agc ggg ctc ttt aag gcc aag cag tgc aac ggc
Pro Asp Cys Asp Glu Ser Gly Leu Phe Lys Ala Lys Gln Cys Asn Gly
                                                                                                  336
                                       80
                                                                 85
       acc tcc acg tgc tgg tgt gtg aac act gct ggg gtc aga aga aca gac
Thr Ser Thr Cys Trp Cys Val Asn Thr Ala Gly Val Arg Arg Thr Asp
90 95 100 105
                                                                                                  384
       aag gac act gaa ata acc tgc tct gag cga gtg aga acc tac tgg atc
Lys Asp Thr Glu Ile Thr Cys Ser Glu Arg Val Arg Thr Tyr Trp Ile
                                                                                                  432
                            110
                                                      115
                                                                                                  480
       atc att gaa cta aaa cac aaa gca aga gaa aaa cct tat gat agt aaa
       Ile Ile Glu Leu Lys His Lys Ala Arg Glu Lys Pro Tyr Asp Ser Lys
                                                 13Ŏ
                                                                            135
       agt ttg cgg act gca ctt cag aag gag atc aca acg cgt tat caa ctg
Ser Leu Arg Thr Ala Leu Gln Lys Glu Ile Thr Thr Arg Tyr Gln Leu
                                                                                                  528
                                            145
                                                                      150
                                                                                                  576
       gat cca aaa ttt atc acg agt att ttg tat gag aat aat gtt atc act
       Åsp Pro Lys Phe Ile Thr Ser Ile Leu Tyr Glu Asn Asn Val Ile Thr
            155
                                       160
                                                                 165
       att gat ctg gtt caa aat tct tct caa aaa act cag aat gat gtg gac
Ile Asp Leu Val Gln Asn Ser Ser Gln Lys Thr Gln Asn Asp Val Asp
                                                                                                  624
       170
                                 175
                                                           180
       ata gct gat gtg gct tat tat ttt gaa aaa gat gtt aaa ggt gaa tcc
                                                                                                  672
       Ile Ala Asp Val Ala Tyr Tyr Phe Glu Lys Asp Val Lys Gly Glu Ser
                                                      195
                            190
                                                                                                  720
       ttg ttt cat tct aag aaa atg gac ctg aca gta aat ggg gaa caa ctg
       Leu Phe His Ser Lys Lys Met Asp Leu Thr Val Asn Gly Glu Gln Leu
                       205
                                                 210
       gat ctg gat cct ggt caa act tta att tat tat gtt gat gaa aaa gca
Asp Leu Asp Pro Gly Gln Thr Leu Ile Tyr Tyr Val Asp Glu Lys Ala
                                                                                                  768
                                            225
                                                                      230
                                                                                                  816
       cct gaa ttc tca atg cag ggt cta aaa gct ggt gtt att gct gtt att
       Pro Glu Phe Ser Met Gln Gly Leu Lys Ala Gly Val Ile Ala Val Ile
                                       240
```

Page 32

```
gtg gtt gtg gtg ata gca gtt gtt gct gga att gtt gtg ctg gtt att val val val Ile Ala Val Val Ala Gly Ile Val Val Leu Val Ile
       250
                             255
                                                    260
      tcc aga aag aga atg gca aag tat gag aag gct gag ata aag gag
Ser Arg Lys Lys Arg Met Ala Lys Tyr Glu Lys Ala Glu Ile Lys Glu
                                                                       280
                         270
                                                275
       atg ggt gag atg cat agg gaa ctc aat gca taa
      Met Gly Glu Met His Arg Glu Leu Asn Ala
                                           290
<210> 56
<211> 314
<212> PRT
<213> Homo sapiens
<400> 56
      Met Ala Pro Pro Gln Val Leu Ala Phe Gly Leu Leu Ala Ala Ala
                                            -15
      Thr Ala Thr Phe Ala Ala Ala Gln Glu Glu Cys Val Cys Glu Asn Tyr
                                 -1 1
              -5
      Lys Leu Ala Val Asn Cys Phe Val Asn Asn Asn Arg Gln Cys Gln Cys 10 20 25
      Thr Ser Val Gly Ala Gln Asn Thr Val Ile Cys Ser Lys Leu Ala Ala
                         30
                                               35
       Lys Cys Leu val Met Lys Ala Glu Met Asn Gly Ser Lys Leu Gly Arg
                                           50
      Arg Ala Lys Pro Glu Gly Ala Leu Gln Asn Asn Asp Gly Leu Tyr Asp 60 65 70
      Pro Asp Cys Asp Glu Ser Gly Leu Phe Lys Ala Lys Gln Cys Asn Gly
                                 80
      Thr Ser Thr Cys Trp Cys Val Asn Thr Ala Gly Val Arg Arg Thr Asp 90 95 100 105
      Lys Asp Thr Glu Ile Thr Cys Ser Glu Arg Val Arg Thr Tyr Trp Ile
110 _ _ 115 120
      Ile Ile Glu Leu Lys His Lys Ala Arg Glu Lys Pro Tyr Asp Ser Lys
125 130 135
                    125
      Ser Leu Arg Thr Ala Leu Gln Lys Glu Ile Thr Thr Arg Tyr Gln Leu
                                      145
                                                             150
               140
       Asp Pro Lys Phe Ile Thr Ser Ile Leu Tyr Glu Asn Asn Val Ile Thr
                                  160
      Ile Asp Leu Val Gln Asn Ser Ser Gln Lys Thr Gln Asn Asp Val Asp
                             175
                                                    180
       Ile Ala Asp Val Ala Tyr Tyr Phe Glu Lys Asp Val Lys Gly Glu Ser
                                                195
                         190
      Leu Phe His Ser Lys Lys Met Asp Leu Thr Val Asn Gly Glu Gln Leu
                                           210
                                                                  215
      Asp Leu Asp Pro Gly Gln Thr Leu Ile Tyr Tyr Val Asp Glu Lys Ala
                                                             230
               220
                                      225
      Pro Glu Phe Ser Met Gln Gly Leu Lys Ala Gly Val Ile Ala Val Ile
235 240 245
      Val Val Val Val Ile Ala Val Val Ala Gly Ile Val Val Leu Val Ile
250 255 260 265
      Ser Arg Lys Lys Arg Met Ala Lys Tyr Glu Lys Ala Glu Ile Lys Glu
                        27Ŏ
                                               275
      Met Gly Glu Met His Arg Glu Leu Asn Ala
<210> 57
<211> 26
<212> DNA
<213> Homo sapiens
<220>
```

864

912

945

```
<221> misc_feature
<223> Forward Primer (for both soluble and full length Ep-CAM): EC-1
<400> 57
                                                                               26
      ttatgtcgac agcatggcgc ccccgc
<210> 58
<211> 31
<212> DNA
<213> Homo sapiens
<220>
<221> misc_feature
<223> Ep-CAM Reverse Primer (for soluble Ep-CAM): EC-2
<400> 58
                                                                               31
      gagttacgtc ccagatttta ttgggccccc t
<210> 59
<211> 30
<212> DNA
<213> Homo sapiens
<220>
<221> misc_feature
<223> Ep-CAM Reverse Primer (for full-length Ep-CAM): EC-3
<400> 59
                                                                               30
      gtatcccttg agttacgtat tgagctcgtt
<210> 60
<211> 112
<212> PRT
<213> Homo sapiens
<220>
<221> MISC_FEATURE
<223> Variable Region for Mouse-Human Chimeric ING-1 Light Chain
Asp Ile Val Met Thr Gln Ala Ala Phe Ser Asn Pro Val Thr Leu Gly
Thr Ser Gly Ser Ile Ser Cys Arg Ser Ser Lys Ser Leu Leu His Ser 20 25 30
Asn Gly Ile Thr Tyr Leu Tyr Trp Tyr Leu Gln Lys Pro Gly Gln Ser
Pro Gln Leu Leu Ile Tyr Gln Met Ser Asn Leu Ala Ser Gly Val Pro
Asp Arg Phe Ser Ser Ser Gly Ser Gly Thr Asp Phe Thr Leu Arg Ile 65 70 75 80
Ser Arg Val Glu Ala Glu Asp Val Gly Val Tyr Tyr Cys Ala Gln Asn
                                        Page 34
```

95

Leu Glu Leu Pro Arg Thr Phe Gly Gly Gly Thr Lys Leu Glu Met Lys $100 \hspace{1cm} 105 \hspace{1cm} 110$

<210> 61 <211> 116

<212> PRT

<213> Homo sapiens

<220>

<221> MISC_FEATURE

<223> Variable Region for Mouse-Human Chimeric ING-1 Heavy Chain

<400> 61

Gln Ile Gln Leu Val Gln Ser Gly Pro Glu Leu Lys Lys Pro Gly Glu 1 5 10 15

Thr Val Lys Ile Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Lys Tyr 20 25 30

Gly Met Asn Trp Val Lys Gln Ala Pro Gly Lys Gly Leu Lys Trp Met 35 40 45

Gly Trp Ile Asn Thr Tyr Thr Glu Glu Pro Thr Tyr Gly Asp Asp Phe 50 60

Lys Gly Arg Phe Ala Phe Ser Leu Glu Thr Ser Ala Ser Thr Ala Asn 65 70 75 80

Leu Gln Ile Asn Asn Leu Lys Ser Glu Asp Thr Ala Thr Tyr Phe Cys 85 90 95

Ala Arg Phe Gly Ser Ala Val Asp Tyr Trp Gly Gln Gly Thr Ser Val 100 105 110

Thr Val Ser Ser 115